

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

# OM protein - protein search, using sw model

Run on: August 29, 2005, 19:09:53 ; Search time 99 Seconds  
(without alignments)  
4570.805 Million cell updates/sec

Title: US-09-945-265-2

Perfect score: 6106

Sequence: 1 MKDSCITVMAMALLSGFFFF.....DPGLKPLHEKDSGGGKD 1170

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: Geneseqp19808:\*

2: Geneseqp19908:\*

3: Geneseqp20008:\*

4: Geneseqp20018:\*

5: Geneseqp20028:\*

6: Geneseqp20038:\*

7: Geneseqp20048:\*

8: Geneseqp20058:\*

9: Geneseqp20068:\*

10: Geneseqp20078:\*

11: Geneseqp20088:\*

12: Geneseqp20098:\*

13: Geneseqp20108:\*

14: Geneseqp20118:\*

15: Geneseqp20128:\*

16: Geneseqp20138:\*

17: Geneseqp20148:\*

18: Geneseqp20158:\*

19: Geneseqp20168:\*

26 5533.5 90.6 1065 2 AAW35852  
27 5533.5 90.6 1065 6 ABU05074  
28 3450 56.5 681 8 ADH18885  
29 3066 50.2 589 8 ADO43838  
30 1565 25.6 1153 2 AAR04136  
31 1563.5 25.6 1152 8 ADP12435  
32 1563 25.6 1153 2 AAW65090  
33 1563 25.6 1153 2 AAB07360  
34 1563 25.6 1153 5 AAB08052  
35 1563 25.6 1153 5 ABG61469  
36 1563 25.6 1153 5 AAO14428  
37 1563 25.6 1153 7 ADD25615  
38 1563 25.6 1153 8 ADR23250  
39 1562.5 25.6 1152 8 ADM93589  
40 1522.5 24.9 1163 8 ADP44061  
41 1521.5 24.9 1163 8 ADN02004  
42 1521.5 24.9 1163 8 ADQ17510  
43 1515.5 24.8 1163 6 ABU07406  
44 1515.5 24.8 1163 7 ADG32005  
45 1511.5 24.8 1163 2 AAR07120

## ALIGNMENTS

RESULT 1  
ID AAW80251 standard; protein; 1170 AA.

AC AAW80251;

DT 15-JUN-2002 (first entry)

DE Human integrin 1 alpha-L subunit protein.

XX Integrin; antiinflammatory; immunosuppression; nephritis; dermatitis;

KW inflammatory disease; autoimmune disorder; Crohn's disease;

KW human immunodeficiency virus; HIV; myocardial infarction;

KW Sjorgen's syndrome; rheumatoid arthritis.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 214 /note= "Encoded by TGG"

XX W0200218583-A2.

ED 07-MAR-2002.

XX 31-AUG-2001; 2001WO-US027227.

PF 01-SEP-2000; 2000US-0229700P.

PR (BL00-) CENT BLOOD RES INC.

PI Springer TA, Shimoaka M, Lu C;

XX WPI; 2002-382964/41.

DR N-PSDB; ABR50045.

XX Modified integrin-I or integrin I-like domain polypeptide useful as an

PT immunogen to produce antibodies specific to polypeptide, comprises a

PT disulfide bond such that polypeptide is stabilized in a desired

PT conformation.

XX Disclosure; Page 105-108; 112pp; English.

XX This invention relates to a modified integrin-I or integrin I-like domain

XX polypeptide comprising at least one disulfide bond so that the domain is

XX stabilised in a desired conformation. The polypeptide of the invention

XX may have antiinflammatory or immunosuppressive activities. The

XX polypeptides of the invention have an open conformation and are useful as

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6106	100.0	1170	5	AAU80251 Human int
2	6106	100.0	1170	6	ABU05077 Human exp
3	6106	100.0	1170	6	AAO30992 Human int
4	6106	100.0	1170	8	ADM99587 Human int
5	6098	99.9	1170	2	AAR80107 LFA-1 alp
6	6098	99.9	1170	5	ABB76377 Lymphocyt
7	6098	99.9	1170	6	ABU05076 Human exp
8	6098	99.9	1170	6	ABU05073 Human exp
9	6098	99.9	1170	6	ABU05071 Human exp
10	6098	99.9	1170	8	ADO43837 Human Lym
11	6098	99.9	1170	8	ADP12998 Protein e
12	6098	99.9	1170	8	ADQ39425 Human myo
13	6072	99.4	1170	2	AAR05782 LFA-1 alp
14	6061.5	99.3	1223	3	ADQ39423 Human myo
15	6053.5	99.1	1223	6	ABU05070 Human exp
16	6053.5	99.1	1223	7	ADJ68489 Human hea
17	5973	97.8	1145	6	AAU03973 Alpha L c
18	5973	97.8	1145	6	ABU05072 Human exp
19	5649.5	92.5	1086	2	AAW81839 Human LFA
20	5649.5	92.5	1086	6	ABU05078 Human exp
21	5585	91.5	1086	6	ABU05075 Human exp
22	5585	91.5	1086	6	ABU05069 Human exp
23	5585	91.5	1086	6	AAO30991 Human int
24	5585	91.5	1086	7	ADJ70065 Human hea
25	5585	91.5	1086	8	ADQ39424 Human myo

CC immunogens to produce antibodies that selectively bind to integrin I-  
CC domain; and for identifying a modulator of integrin activity, or of  
CC interaction of an integrin and a cognate ligand. The polypeptide of the  
CC invention, or antibodies (preferably anti- $\alpha$ -1 antibody) is useful for  
CC treating or preventing an integrin mediated disorder which is an  
CC inflammatory or autoimmune disorder in a subject and for inhibiting the  
CC binding of an integrin to a cognate ligand in a subject. A therapeutic  
CC composition comprising the peptide of the invention is useful for  
CC creating an integrin mediated disorder such as Crohn's disease, nephritis  
CC ; human immunodeficiency virus (HIV), myocardial infarction, Sjogren's  
CC syndrome, rheumatoid arthritis, dermatitis. The polypeptides and/or  
CC active or antigenic fragments are useful as reagents for diagnosis of  
CC integrin-mediated disorders. The present sequence represents the human  
CC polypeptides of the invention  
XX  
SQ Sequence 1170 AA;  
Query Match 100.0%; Score 6106; DB 5; Length 1170;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKDSCTTMMAMALLSGFFFPAPASSYNLDVVGARSFSPRRGRHRYVLDVNGVYGA 60  
DB 1 MKDSCTTMMAMALLSGFFFPAPASSYNLDVVGARSFSPRRGRHRYVLDVNGVYGA 60  
QY PGEAGNSTSLYQCGSGTGHCLPTLRLGASNTSKYLGMTLADPTDGSLLACDPGLSRTCD 120  
DB PGEAGNSTSLYQCGSGTGHCLPTLRLGASNTSKYLGMTLADPTDGSLLACDPGLSRTCD 120  
QY 121 QNTYLSGLCYLFRONTQGPMLQGRPGQECIKGNVDLVELFDGSMSLQPDFOKILDFMK 180  
DB 121 QNTYLSGLCYLFRONTQGPMLQGRPGQECIKGNVDLVELFDGSMSLQPDFOKILDFMK 180  
QY 181 DVMKTLSTSYQPAANVQSTSYKTRPDSYVKKRDPALLKHYKAMLLNTTGALNV 240  
DB 181 DVMKTLSTSYQPAANVQSTSYKTRPDSYVKKRDPALLKHYKAMLLNTTGALNV 240  
QY 241 ATEVFREELGARPRATKVLIIITDGEATDSGNIDAAKQIIIRYIIIGIGHFQTKXSQETLH 300  
DB 241 ATEVFREELGARPRATKVLIIITDGEATDSGNIDAAKQIIIRYIIIGIGHFQTKXSQETLH 300  
QY 301 KFAKSPASEFVKIILDFEKLKDLFTELQKKIYVIGTSKODLTSFNNELSSSGISADLSR 360  
DB 301 KFAKSPASEFVKIILDFEKLKDLFTELQKKIYVIGTSKODLTSFNNELSSSGISADLSR 360  
QY 361 GHAVVGAAGADWAGGFIDLKADLODFTFIGNEPITPEVRAGYLGYYTWMPSRQKTSLL 420  
DB 361 GHAVVGAAGADWAGGFIDLKADLODFTFIGNEPITPEVRAGYLGYYTWMPSRQKTSLL 420  
QY 421 ASGARPRYOHMGRVLLFOEPQGGHMSQVQTIHGTOIGSFPGSBLCGVVDODGETELLII 480  
DB 421 ASGARPRYOHMGRVLLFOEPQGGHMSQVQTIHGTOIGSFPGSBLCGVVDODGETELLII 480  
QY 481 GAPPFYGEORGRVFIYQRRQLGFEVEVELQGDPRYPLGRGEAITALTDINGDLVDVA 540  
DB 481 GAPPFYGEORGRVFIYQRRQLGFEVEVELQGDPRYPLGRGEAITALTDINGDLVDVA 540  
QY 541 VGAPLEBOGAVYITNGRHGSLSPDSQRIBESTOVLSGIQMTGRSIGHGVKLESGGLADVA 600  
DB 541 VGAPLEBOGAVYITNGRHGSLSPDSQRIBESTOVLSGIQMTGRSIGHGVKLESGGLADVA 600  
QY 601 VGASOMTVLSRPVMDVTLMSFSPAIPIVHEVCSTSNKMKKEGNITICQOISLY 660  
DB 601 VGASOMTVLSRPVMDVTLMSFSPAIPIVHEVCSTSNKMKKEGNITICQOISLY 660  
QY 661 POFQGRVLANLTLYTLQDGHRTTRRGLPPGGRHELRRIATYTSMSCTDFSFHPVCYOD 720  
DB 661 POFQGRVLANLTLYTLQDGHRTTRRGLPPGGRHELRRIATYTSMSCTDFSFHPVCYOD 720  
QY 721 LISPINVSLNLSWEEBGTTPDQAKODIPILRPSLHSTWEIPEFKNGCEDKCKEAN 780  
DB 721 LISPINVSLNLSWEEBGTTPDQAKODIPILRPSLHSTWEIPEFKNGCEDKCKEAN 780

QY 781 LRVSFSPARSALRLTFAPASLYVELSTSNLEBDAYWVQDLHPPGGSFPAKVEMLKPHSQ 840  
DB 781 LRVSFSPARSALRLTFAPASLYVELSTSNLEBDAYWVQDLHPPGGSFPAKVEMLKPHSQ 840  
QY 841 IPVSCBELPEESRLSRLSALSCNVSPIFKAGSHVALQMMFNTLVNSWGDSVELHANVTC 900  
DB 841 IPVSCBELPEESRLSRLSALSCNVSPIFKAGSHVALQMMFNTLVNSWGDSVELHANVTC 900  
QY 901 MNESDLENSATTTIPIIYINILLOQEDSTLVVSFPPKPKIHQVHMVQVRQPS 960  
DB 901 MNESDLENSATTTIPIIYINILLOQEDSTLVVSFPPKPKIHQVHMVQVRQPS 960  
QY 961 IHDNIFTLBAVVGVPQPPSEGPITTHQMSVQMPVPCHYEDLERLPDAEPCLPGALFR 1020  
DB 961 IHDNIFTLBAVVGVPQPPSEGPITTHQMSVQMPVPCHYEDLERLPDAEPCLPGALFR 1020  
QY 1021 CPVVFROEILVQYIGTLELVEGEIEASSMFSLCSSLISFNSXGFHLVGSNASLAQVVMK 1080  
DB 1021 CPVVFROEILVQYIGTLELVEGEIEASSMFSLCSSLISFNSXGFHLVGSNASLAQVVMK 1080  
QY 1081 VDVVYERQMLLYLVLSGIGLLLLIFLYLVYVGFPRKRLKERMAGRGVPGIPEADS 1140  
DB 1081 VDVVYERQMLLYLVLSGIGLLLLIFLYLVYVGFPRKRLKERMAGRGVPGIPEADS 1140  
QY 1141 EQLASQGEADPGCLKPIHEKDESGGKGD 1170  
DB 1141 EQLASQGEADPGCLKPIHEKDESGGKGD 1170  
RESULT 2  
ABU05077  
ID ABU05077 standard; protein; 1170 AA.  
XX  
AC ABU05077;  
XX  
DT 29-JAN-2003 (first entry)  
XX  
DE Human expressed protein tag (EPT) #1743.  
XX  
KW Translational profiling; expressed protein tag; EPT, kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
XX  
OS Homo sapiens.  
XX  
PN W0200278524-A2.  
XX  
PD 10-OCT-2002.  
XX  
PE 28-MAR-2002; 2002MO-US009671.  
XX  
PR 28-MAR-2001; 2001US-0279495P.  
PR 21-MAY-2001; 2001US-0292544P.  
PR 08-AUG-2001; 2001US-0310801P.  
PR 01-OCT-2001; 2001US-0326370P.  
PR 04-DEC-2001; 2001US-0336780P.  
PR 20-FEB-2002; 2002US-0358985P.  
XX  
PA (ZYCO-) ZYCO5 INC.  
XX  
PI Chicx RM, Tomlinson AJ, Urban RG;  
XX  
DR WPI; 2003-040607/03.  
XX  
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
XX cytoskeletal proteins, receptors or transcription factors), useful for  
XX treating cancer; e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
XX leukemia.  
XX  
XX Example 2; SEQ ID NO 1743; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX

Query Match	100.0%;	Score 6106;	DB 6;	Length 1170;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1170; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

Qy	1	MOSCIITVMMALLSGFFFPAPASSVNLIVRABSFSPPRAGRHNRYVLOVNGVTVGA	60
Db	1	MKOSCIITVMMALLSGFFFPAPASSVNLIVRABSFSPPRAGRHNRYVLOVNGVTVGA	60
Qy	61	PGABNSYGSILYQOQSQTGHCLPVTLRGNSYTSKYTGAMTLADPTDGSILACDPGLSRTCD	120
Db	61	PGABNSYGSILYQOQSQTGHCLPVTLRGNSYTSKYTGAMTLADPTDGSILACDPGLSRTCD	120
Qy	121	QNTYLSGLCYLFFRONLQOPMLQGRPGQBOECIKGNVDVFLFPDGSMSLOPDEFOKILDFMK	180
Db	121	QNTYLSGLCYLFFRONLQOPMLQGRPGQBOECIKGNVDVFLFPDGSMSLOPDEFOKILDFMK	180
Qy	181	DVKKLSNYSYQPAAVQSTSYKTEPESBDYVYKRODPALEKHYKMLLTNTFGAINTV	240
Db	181	DVKKLSNYSYQPAAVQSTSYKTEPESBDYVYKRODPALEKHYKMLLTNTFGAINTV	240
Qy	241	ATVPPEELGARPDARKVLIITTDGANDSGNIDAKOIRIYIIGIGHPTKSSOETLH	300
Db	241	ATVPPEELGARPDARKVLIITTDGANDSGNIDAKOIRIYIIGIGHPTKSSOETLH	300
Qy	301	KFASKKPASEEVKILDFPEFKIDLFTESLOKIVIEBGTSKODLTFSPNMLSAGISADLSR	360
Db	301	KFASKKPASEEVKILDFPEFKIDLFTELOKIVIEBGTSKODLTFSPNMLSAGISADLSR	360
Qy	361	GHAVGAVGAKDWAAGFLDKADLODDPTIGNEPLTPREVAGYLGYYTVMPSROKTSLL	420
Db	361	GHAVGAVGAKDWAAGFLDKADLODDPTIGNEPLTPREVAGYLGYYTVMPSROKTSLL	420
Qy	421	ASGAPRYQHKRGVLFQEPQGGGSHMSQVOTIHGTOIGSYFGEELCGVDVDGGETELL	480
Db	421	ASGAPRYQHKRGVLFQEPQGGGSHMSQVOTIHGTOIGSYFGEELCGVDVDGGETELL	480
Qy	481	GAPLFFGEQGGGVFLYQRRQLGFEVBSLSQDPEYPLGRGEBALTALTDINGGLDVA	540
Db	481	GAPLFFGEQGGGVFLYQRRQLGFEVBSLSQDPEYPLGRGEBALTALTDINGGLDVA	540
Qy	541	VGAPLEBOGAVYTFNHRHGLSPQSPQRLEGQVLSGIQMFGRSITHGVLOEBGGLADVA	600
Db	541	VGAPLEBOGAVYTFNHRHGLSPQSPQRLEGQVLSGIQMFGRSITHGVLOEBGGLADVA	600
Qy	601	VGABSQMTVLSSRPVDMVTLMSPSPABIPVHEVCSYSTSNKKKEGVNITTCFOIKSLY	660
Db	601	VGABSQMTVLSSRPVDMVTLMSPSPABIPVHEVCSYSTSNKKKEGVNITTCFOIKSLY	660
Qy	661	POQQRVYVNLTYTLODGHTRRRRLPFGGHELRNRIAVTTSMSCTDPSFHPVYVOD	720
Db	661	POQQRVYVNLTYTLODGHTRRRRLPFGGHELRNRIAVTTSMSCTDPSFHPVYVOD	720

QY	721	LISPIANSLNLSWEEESTPRPDQKQKDIPILIRPSLHSETWEI	PPEKNCQSDKKCEAN	780
Db	721	LISPIANSLNLSWEEESTPRDQKQKDIPILIRPSLHSETWEI	PPEKNCQSDKKCEAN	780
QY	781	LRVSPSPARSRALRLTAVASLSVBLSLSNLEBDAYWQJDLHPGSLSRKYEMLKPHSQ		840
Db	781	LRVSPSPARSRALRLTAVASLSVBLSLSNLEBDAYWQJDLHPGSLSRKYEMLKPHSQ		840
QY	841	IPVSCCEILPESSRLLSRALSCNVSSPIPKAGHSVALQMMFNTLVNNSWGDSTVELHANTVC	900	
Db	841	IPVSCCEILPESSRLLSRALSCNVSSPIPKAGHSVALQMMFNTLVNNSWGDSTVELHANTVC	900	
QY	901	NNEBSDLLEDSATTIIPILYPIINLIQDOEDSTLYLVSFTPKGPKIHQVKNMYQVRIQPS	960	
Db	901	NNEBSDLLEDSATTIIPILYPIINLIQDOEDSTLYLVSFTPKGPKIHQVKNMYQVRIQPS	960	
QY	961	IHDNIPTLEAVGVGPDPSPSGPIPTHQNSVQMEPPVCHYEDLERI	PDAEPCLPQALFR	102
Db	961	IHDNIPTLEAVGVGPDPSPSGPIPTHQNSVQMEPPVCHYEDLERI	PDAEPCLPQALFR	102
QY	1021	CPVVPFROEIIQOVITGLTELVEGIEEASSMFSICSSLISTFNSKXHLVGSNNSLQAVWNK	108	
Db	1021	CPVVPFROEIIQOVITGLTELVEGIEEASSMFSICSSLISTFNSKXHLVGSNNSLQAVWNK	108	
QY	1081	VDVYYEKQMLTYLYLSGIGJLLLLLLFIIVLYKYGFFRKRLKEKREAGRGVNGIIPAEDS	114	
Db	1081	VDVYYEKQMLTYLYLSGIGJLLLLLLFIIVLYKYGFFRKRLKEKREAGRGVNGIIPAEDS	114	
QY	1141	EQLASGQDAGDPGCLKPLHEKDSBSGGGKD	1170	
Db	1141	EQLASGQDAGDPGCLKPLHEKDSBSGGGKD	1170	

RESULT 3  
AAO30992  
ID AAO30992 standard; protein; 1170 AA

AC AA030992;

DT 06-OCT-2003 (first entry)

DE Human integrin alpha-L protein #2.

KM Human; integrin alpha-1; haematological; central nervous system; CNS;  
KM gastrointestinal; gene therapy; chronic obstructive pulmonary disorder  
KM COPD; cardiovascular disorder; asthma; chromosome 16p11.2.

OS Homo sapiens.

FH	Key	Location/Qualifiers

/note= "Encoded by ATG"

FT /note= "Encoded by TTGT

```
FT, /note= "Encoded by ATC"
```

```

FT      /note= "Encoded by GCGGGG
YY

```

PN WO2003051924-A1  
XX

26-JUN-2003  
PD  
XX

17-DEC-2002; 2002MC-EF014381  
XX

PR 09-JUL-2002; 2002US-0394246P

PA (FARB ) BAYER AG.

PI Smolyar A

DR WPI; 2003-533001/50.

DR N-PSDB; AAL62479.

XX New integrin alpha-L polypeptide or polynucleotide, useful for preparing  
PT a composition for treating hematological, gastrointestinal, CNS or  
PT cardiovascular disorder, asthma or COPD.

XX Claim 1; Page 106-108; 121pp; English.

XX The invention relates to human integrin alpha-L protein and its nucleic  
CC acid sequence. Integrin alpha-L DNA is used to prepare a composition for  
CC treating hematological, gastrointestinal, central nervous system (CNS)  
CC or cardiovascular disorder, asthma or chronic obstructive pulmonary  
CC disorder (COPD). It is also used in gene therapy. The present sequence is  
CC human integrin alpha-L protein. Human integrin alpha-L gene is located at  
CC chromosome 16p11.2

XX Sequence 1170 AA;

Query Match 100.0%; Score 6106; DB 6; Length 1170;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKDSCITVMAMALLSGFFFPASSYNLDVGAASFSPRRGRHGRVLYGVNGVITYGA 60  
Db 1 MKDSCITVMAMALLSGFFFPASSYNLDVGAASFSPRRGRHGRVLYGVNGVITYGA 60  
QY PGEAGNSTSLYQCCSGTGCHLPTVLRGSNTSKYLGMTLADPDGSLIACDPGLSPTCD 120  
Db 61 PGEAGNSTSLYQCCSGTGCHLPTVLRGSNTSKYLGMTLADPDGSLIACDPGLSPTCD 120  
QY 121 QNTYLSGLCYLFRONTLQGPMLQGRPGQECIKGNVDLFLFDGSMSLQPDFQKILDFMK 180  
Db 121 QNTYLSGLCYLFRONTLQGPMLQGRPGQECIKGNVDLFLFDGSMSLQPDFQKILDFMK 180  
QY 181 DVMKKLSNTSQPAAVGOSTSYKTEPFDSDYKRDPAALLKHYKMLLNTTGALINY 240  
Db 181 DVMKKLSNTSQPAAVGOSTSYKTEPFDSDYKRDPAALLKHYKMLLNTTGALINY 240  
QY 241 ATVEFBEELGARPATKVLIIITDGEATDSGNIDAAKIIIRYIGIGHPOTKSOETLH 300  
Db 241 ATVEFBEELGARPATKVLIIITDGEATDSGNIDAAKIIIRYIGIGHPOTKSOETLH 300  
QY 301 KFAKSPASEFVKIIDTFEKLKDLFTELQKIIYIEGTSKODLTSPNMLSSSGISADLSR 360  
Db 301 KFAKSPASEFVKIIDTFEKLKDLFTELQKIIYIEGTSKODLTSPNMLSSSGISADLSR 360  
QY 361 GHAVVAVGADWAGGFLDLKADLDDTFIGNBPLTPVRAGYLGYYTWMPSRQKISL 420  
Db 361 GHAVVAVGADWAGGFLDLKADLDDTFIGNBPLTPVRAGYLGYYTWMPSRQKISL 420  
QY 421 ASGA.PRYOHMGRVLLFOBPQGGHMSOVQTIHGTOIGSYFGSELGVVDDGFEELLII 480  
Db 421 ASGA.PRYOHMGRVLLFOBPQGGHMSOVQTIHGTOIGSYFGSELGVVDDGFEELLII 480  
QY 481 GAPLFYGEORGRVFTYORQLGFEVSELQDPPYPLGRFGAITALTDINGDLVDVA 540  
Db 481 GAPLFYGEORGRVFTYORQLGFEVSELQDPPYPLGRFGAITALTDINGDLVDVA 540  
QY 541 VGAPLEBEGAVYITNGRHGGLSPQPSQRIEQTOUTSGIQMGKRSIHGYKDLBEGDLADVA 600  
Db 541 VGAPLEBEGAVYITNGRHGGLSPQPSQRIEQTOUTSGIQMGKRSIHGYKDLBEGDLADVA 600  
QY 601 VGASQMTVLSRPVDMVTLMSPAPRIPVHVECSYSTSNKMEGVNITTCPOIKSLY 660  
Db 601 VGASQMTVLSRPVDMVTLMSPAPRIPVHVECSYSTSNKMEGVNITTCPOIKSLY 660  
QY 661 POFQGRVAVNTLYTLQDGHRTTRRGLPPGGRHLELRNIATVTSNCTDFSFHPVAVQD 720  
Db 661 POFQGRVAVNTLYTLQDGHRTTRRGLPPGGRHLELRNIATVTSNCTDFSFHPVAVQD 720  
QY 721 LISPIVNSLNSLMBEETPRDQAKQDQIPILRPSLSHSTWELPFEKNGCEDKCKEAN 780  
Db 721 LISPIVNSLNSLMBEETPRDQAKQDQIPILRPSLSHSTWELPFEKNGCEDKCKEAN 780

QY 781 LRVSFSPARALRLTAPASLSEYLSLNLSEADAYWVQDLHPFPGLSFRKVEMLKPSHQ 840  
Db 781 LRVSFSPARALRLTAPASLSEYLSLNLSEADAYWVQDLHPFPGLSFRKVEMLKPSHQ 840  
QY 841 IPVSCBELPEESRLSRALSCNVSSPIFKAGHSVALQMMNTLVNSSWGDSEVLIHANTC 900  
Db 841 IPVSCBELPEESRLSRALSCNVSSPIFKAGHSVALQMMNTLVNSSWGDSEVLIHANTC 900  
QY 901 NNEBSDLLENSATTTIPILYINILIQODEDSTLYSFTPKPKKHQVHMVQVRQPS 960  
Db 901 NNEBSDLLENSATTTIPILYINILIQODEDSTLYSFTPKPKKHQVHMVQVRQPS 960  
QY 961 IHDNIPITLBAVVGVPQPEEGPITHOWSQVMEPPVCHIEDLERLPDAEPLCPGALFR 1020  
Db 961 IHDNIPITLBAVVGVPQPEEGPITHOWSQVMEPPVCHIEDLERLPDAEPLCPGALFR 1020  
QY 1021 CPVVFROEILVQVIGTLELVGEIEASMFSLCSSLSISFNSKHFHLVGSNASTLAQVVMK 1080  
Db 1021 CPVVFROEILVQVIGTLELVGEIEASMFSLCSSLSISFNSKHFHLVGSNASTLAQVVMK 1080  
QY 1081 VDVVYERQMLYLYLSGIGILLILLIFLYLYVGVGPKRMLKEMAGRGVPGIPAEBS 1140  
Db 1081 VDVVYERQMLYLYLSGIGILLILLIFLYLYVGVGPKRMLKEMAGRGVPGIPAEBS 1140  
QY 1141 EQLASQGEADPGCLKPLHEKDSRSGGKD 1170  
Db 1141 EQLASQGEADPGCLKPLHEKDSRSGGKD 1170

RESULT 4  
ADM99587 standard; protein; 1170 AA.  
ID ADM99587;  
AC ADM99587;  
DC 17-JUN-2004 (first entry)  
DE Human integrin alphaL subunit precursor protein.  
E human integrin alpha subunit; beta; antipeptidic; thrombolytic; anticoagulant;  
F osteopathic; cyostatic; immunosuppressive; antiinflammatory;  
G neuroprotective; antiskling; immunotherapy; inflammatory;  
H autoimmune disorder; thrombosis; cancer; osteoporosis;  
I sickle cell anaemia; psoriasis; multiple sclerosis; human; alphaL;  
J precursor.  
K Homo sapiens.  
L OS  
M Key Location/Qualifiers  
N MISC-difference 214 /note= "Encoded by TGG"  
O MO204007530-A2.  
P 22-JAN-2004.  
Q 17-JUL-2003; 2003MO-US022301.  
R 17-JUL-2002; 2002US-0396783P.  
S 17-JUL-2002; 2002US-0396790P.  
T 11-SEP-2002; 2002US-0410135P.  
U (BL00-) CENT BLOOD RES INC.  
V Springer TA, Takagi J;  
W WPI; 2004-122877/12.  
X N-PSDB; ADM99586.  
Y Novel modified integrin protein having extracellular domains of integrin  
Z alpha and beta subunits or integrin alphaL and betaL subunit, useful for  
treating integrin mediated disorders.



XX Disclosure: SEQ ID NO 2; 232pp; English.  
PS  
XX The invention relates to a novel isolated or recombinant modified  
CC integrin protein having extracellular domains of integrin alpha and beta  
CC subunits where one of the subunits has one or more mutations, an altered  
CC surface feature or an amino acid substitution or internal deletion,  
CC extracellular domain of the integrin beta subunit that comprises a  
CC mutation that alters a non-cysteine residue to cysteine or extracellular  
CC domain of integrin alpha and beta subunits. The polypeptide of the  
CC invention demonstrates antiproteolytic, thrombolytic, anticoagulant,  
CC osteoprotective and anticlotting activities and may be useful for  
CC immunotherapy in order to prevent or treat an integrin-mediated disorder  
CC such as an inflammatory disorder, an autoimmune disorder, thrombosis,  
CC cancer, osteoporosis, sickle cell anaemia, psoriasis and multiple  
CC sclerosis. The current sequence is that of the human integrin alpha  
CC subunit precursor protein of the invention.  
XX  
SQ Sequence 1170 AA;

Query Match 100.0%; Score 6106; DB 8; Length 1170;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSCITWAMALLSGFFPAPASSYNDVRCARSPPRAGRHGYRLQYGVGYVCA 60  
DB 1 MDSCITWAMALLSGFFPAPASSYNDVRCARSPPRAGRHGYRLQYGVGYVCA 60  
QY 61 PGRSGTSLYOCOSGTGHCPLPTLRGSNYTSKYLGMTLATPTDGSILACPGISRTCD 120  
DB 61 PGRSGTSLYOCOSGTGHCPLPTLRGSNYTSKYLGMTLATPTDGSILACPGISRTCD 120  
QY 121 QNTYLSGLCYLFRONLQGPMLQGRPGFQECIKGNVLYLFDGSMNLQPDFQKILDFMK 180  
DB 121 QNTYLSGLCYLFRONLQGPMLQGRPGFQECIKGNVLYLFDGSMNLQPDFQKILDFMK 180  
QY 181 DVMKGLSNTSYOPAAVQSTSYKTEPDSYKYRKDPDALLGHVGMILLNTFPAINYV 240  
DB 181 DVMKGLSNTSYOPAAVQSTSYKTEPDSYKYRKDPDALLGHVGMILLNTFPAINYV 240  
QY 241 ATAVFREELGAPDPAATKVLIIITDGPATDSGNIDAKDIIIRYIIGKHFQKESQETIH 300  
DB 241 ATAVFREELGAPDPAATKVLIIITDGPATDSGNIDAKDIIIRYIIGKHFQKESQETIH 300  
QY 301 KEASKPASEFVKILDTFEKLDLFTLEOKKIYIVIEGTSKODLTSFMELSSSGISADLSR 360  
DB 301 KEASKPASEFVKILDTFEKLDLFTLEOKKIYIVIEGTSKODLTSFMELSSSGISADLSR 360  
QY 361 GHAVVAVGAKWAGGFLDLKADLDDDTFIGNEPILTPRYAGYLGTYTWMPLPSRQTSLL 420  
DB 361 GHAVVAVGAKWAGGFLDLKADLDDDTFIGNEPILTPRYAGYLGTYTWMPLPSRQTSLL 420  
QY 421 ASDAPRYOMGRVLLFOEPQGGHWSQVTHGTQIGSYFGSELGVVDVDDGKTELLLI 480  
DB 421 ASDAPRYOMGRVLLFOEPQGGHWSQVTHGTQIGSYFGSELGVVDVDDGKTELLLI 480  
QY 481 GAPLFYGEORGRVETIYQRRLGFBEVSELQDPCGYLGRFEBEITALTDINGDGLVYA 540  
DB 481 GAPLFYGEORGRVETIYQRRLGFBEVSELQDPCGYLGRFEBEITALTDINGDGLVYA 540  
QY 541 VGAPLEBOGAVYIFNGRHGGLSPQPSQRIEQTQVLSGIQWFGRSIHGVKDLREGDGLADVA 600  
DB 541 VGAPLEBOGAVYIFNGRHGGLSPQPSQRIEQTQVLSGIQWFGRSIHGVKDLREGDGLADVA 600  
QY 601 VGASOMYIVLSRPVVDWYTLMSFSPARIPVHEVSCVSTSKMEGVNITTCPIKSLY 660  
DB 601 VGASOMYIVLSRPVVDWYTLMSFSPARIPVHEVSCVSTSKMEGVNITTCPIKSLY 660  
QY 661 PQFGRVAVNLTYTLQLDGHRTTRRGLFPGGHRLRNIAVTTNSCTDPSFHPFVQVD 720  
DB 661 PQFGRVAVNLTYTLQLDGHRTTRRGLFPGGHRLRNIAVTTNSCTDPSFHPFVQVD 720

QY 721 LISPINVSLNFSIMEEGTPRDQRAQGDIPILLRPSLSHSETWEIPEKNGCEDKKCEAN 780  
DB 721 LISPINVSLNFSIMEEGTPRDQRAQGDIPILLRPSLSHSETWEIPEKNGCEDKKCEAN 780  
QY 781 LRVSPSPRSBALRTTAPASISVELSLNLEDAAWQDLHFPGLSFRKVEMLKPHSQ 840  
DB 781 LRVSPSPRSBALRTTAPASISVELSLNLEDAAWQDLHFPGLSFRKVEMLKPHSQ 840  
QY 841 IPVSCBELPEBSRLISRALSCNVSSPIFKAGHSVALQMMFNTLVNNSGDSVELHANVTC 900  
DB 841 IPVSCBELPEBSRLISRALSCNVSSPIFKAGHSVALQMMFNTLVNNSGDSVELHANVTC 900  
QY 901 NNEBSDLIEDNSATITIPILPINLIDODSDSTLYSFTKRGKPIHVKMYQVRIQPS 960  
DB 901 NNEBSDLIEDNSATITIPILPINLIDODSDSTLYSFTKRGKPIHVKMYQVRIQPS 960  
QY 961 IHDNHIPTLEAVGVGPQPSSEGPITHQMSVOMEPVPCYEDLERLPPAAEPCLPGALFR 1020  
DB 961 IHDNHIPTLEAVGVGPQPSSEGPITHQMSVOMEPVPCYEDLERLPPAAEPCLPGALFR 1020  
QY 1021 CPVVRQGEILVQVIGTLELVGEIEEASMSFLCSSISISFNSSKPHLYGSNASTLAQVYMK 1080  
DB 1021 CPVVRQGEILVQVIGTLELVGEIEEASMSFLCSSISISFNSSKPHLYGSNASTLAQVYMK 1080  
QY 1081 VDVIYERKQMLTYLXLSGIGILLLLIFIVYKYGFPGKNIKEKMEAGRGVPMNGIPADS 1140  
DB 1081 VDVIYERKQMLTYLXLSGIGILLLLIFIVYKYGFPGKNIKEKMEAGRGVPMNGIPADS 1140  
QY 1141 EQLASQGEAGDPGCLKPLHEKDSBSGGSKD 1170  
DB 1141 EQLASQGEAGDPGCLKPLHEKDSBSGGSKD 1170

RESULT 5  
AAR80107  
ID AAR80107 standard; protein, 1170 AA.

XX AAR80107;

XX 04-MAR-1996 (first entry)

XX LFA-1 alpha subunit CD11a.

XX CD11a; leucocyte function-associated antigen-1; LFA-1; integrin.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Peptide 1..25

XX Region 32..79

XX /label= Repeat

XX /note= "Repeat I"

XX Region 82..132

XX /label= Repeat

XX /note= "Repeat II"

XX Domain 170..349

XX /label= Internal domain

XX /note= "internal domain"

XX Region 339..391

XX /label= Repeat

XX /note= "Repeat III"

XX Region 392..446

XX /label= Repeat

XX /note= "Repeat IV"

XX Region 447..508

XX /label= Repeat

XX /note= "Repeat V"

XX Region 509..567

XX /label= Repeat

XX /note= "Repeat VI"

XX Region 568..629

XX /label= Repeat

```

FT      /note= "Repeat VII"
FT      1089..1112
FT      /label= Trans
FT      /note= "transmembrane domain"
FT      1113..1170
FT      /label= Cyto
FT      /note= "cytoplasmic domain"
XX      MO9528170-A1.
XX      26-OCT-1995.
XX      19-APR-1995; 95WO-US004886.
XX      19-APR-1994; 94US-00229513.
XX      (UNIV ) UNIV KANSAS.
XX      Benedict S, Siahaan TJ, Chan MA, Tibbette SA;
XX      WPI, 1995-373631/48.
XX      Changing peptide reactivity via conjugation with a second peptide -
XX      causes change in conformation of first peptide, pref. Lfa-1 and ICAM-1
XX      functional domain derived peptide(s).
XX      Claim 11; Page 34-37; 64pp; English.
XX      Functional domains derived from LFA-1 alpha subunit CD11a (AAR80107), LFA
XX      -1 beta subunit CD18 (AAR80107) and ICAM-1 CD43 (AAR80110) are used as
XX      the basis of short, synthetic peptides (AAR80109, AAR80111-24) that
XX      modulate ICAM/LFA binding interaction. CD11a is obtd. from human PMA-
XX      stimulated T-lymphocyte HL-60 cells
XX      Sequence 1170 AA:
SQ      Query Match          99.9%; Score 6098; DB 2; Length 1170;
      Best Local Similarity 99.9%; Pred. No. 0;
      Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 MKDSCITTMAMALLSGFFFPAPASYNLDVRGANSFSPRRGRHFGYVLOVGVNGVYGA 60
DB      1 MKDSCITTMAMALLSGFFFPAPASYNLDVRGANSFSPRRGRHFGYVLOVGVNGVYGA 60
QY      61 PEGNGSTSLKOCOSGTGHC.PVTLRGSNYSKYIGMTLADPTDGSITLACDPGLSRTCD 120
DB      61 PEGNGSTSLKOCOSGTGHC.PVTLRGSNYSKYIGMTLADPTDGSITLACDPGLSRTCD 120
QY      121 QNTYLSGLCYLFRONTLQGPMLQGRPGFOECIKGNVDLFLFDGSMSTLOPDEFOKILDFMK 180
DB      121 QNTYLSGLCYLFRONTLQGPMLQGRPGFOECIKGNVDLFLFDGSMSTLOPDEFOKILDFMK 180
QY      181 DVMTKLSTSYQFPAVQSTSYKTEFDSDYVKRQDPALLKHYKAMLLNTTGAINYV 240
DB      181 DVMTKLSTSYQFPAVQSTSYKTEFDSDYVKRQDPALLKHYKAMLLNTTGAINYV 240
QY      241 ATEVFERELGARPDATKVLIIITDGEATDSGNIDAAKQIIRYIIGISGHPOTKSQETLH 300
DB      241 ATEVFERELGARPDATKVLIIITDGEATDSGNIDAAKQIIRYIIGISGHPOTKSQETLH 300
QY      301 KFA$KPA$B$FVKIDTFEKLKDLFTELQKIVLEGT$KODLTSFNMELSSSGISADLSR 360
DB      301 KFA$KPA$B$FVKIDTFEKLKDLFTELQKIVLEGT$KODLTSFNMELSSSGISADLSR 360
QY      361 GHAVVGAIVGADWAGGFLDLKADLDDDTFIGNEPILTEPVRAGYIGYTTWLP$RQKISL 420
DB      361 GHAVVGAIVGADWAGGFLDLKADLDDDTFIGNEPILTEPVRAGYIGYTTWLP$RQKISL 420
QY      421 ASGARVYOHMRVLLFOEPGOGGSHSVOYTIHGQIIGSYFGSELGQVVDODGETELLII 480
DB      421 ASGARVYOHMRVLLFOEPGOGGSHSVOYTIHGQIIGSYFGSELGQVVDODGETELLII 480
QY      481 GAPLFYGEORGRGVFIYQRRLGFEFVSELQDPGYPLGRFGEAITALTIDINGDLVDVA 540
DB      481 GAPLFYGEORGRGVFIYQRRLGFEFVSELQDPGYPLGRFGEAITALTIDINGDLVDVA 540

```

```

DB      481 GAPLFYGEORGRGVFIYQRRLGFEFVSELQDPGYPLGRFGEAITALTIDINGDLVDVA 540
QY      541 VGAFLEBQGAIVYIFNGHGGSLSPQSGRIEQTQVLSGIQWFGS IHKVKLBDGLADVA 600
DB      541 VGAFLEBQGAIVYIFNGHGGSLSPQSGRIEQTQVLSGIQWFGS IHKVKLBDGLADVA 600
QY      601 VGASQMIYLSR$RPVDMTLM$FSPALIPVHEVCSYSTSNMKEGVNTTICFQIKSLY 660
DB      601 VGASQMIYLSR$RPVDMTLM$FSPALIPVHEVCSYSTSNMKEGVNTTICFQIKSLY 660
QY      661 POFQRLVANIYTYTLQDGHRTRRGLFPGRRHRLRNIAVTTSM$CTDPSFHPVVCOD 720
DB      661 POFQRLVANIYTYTLQDGHRTRRGLFPGRRHRLRNIAVTTSM$CTDPSFHPVVCOD 720
QY      721 LISPINVSNLPSLMEEGT$PRDQAOQKQIPLIRP$LSHETWEIIP$KXCGEDKCEAN 780
DB      721 LISPINVSNLPSLMEEGT$PRDQAOQKQIPLIRP$LSHETWEIIP$KXCGEDKCEAN 780
QY      781 LRV$F$PAR$RALRLTAFASL$VEL$SLNLEDAVYVQLDLHFP$GL$FRKVEMLKPH$Q 840
DB      781 LRV$F$PAR$RALRLTAFASL$VEL$SLNLEDAVYVQLDLHFP$GL$FRKVEMLKPH$Q 840
QY      841 IPVSCBELP$BSRL$SRL$CNVSSPIFKAGHSVALQ$MFTNLYNSSWGD$VEIHANVTC 900
DB      841 IPVSCBELP$BSRL$SRL$CNVSSPIFKAGHSVALQ$MFTNLYNSSWGD$VEIHANVTC 900
QY      901 NNEDSDLENSATTTIPIIYPTNILLQDOEDSTLYVSPFKPKTHQVHMYOVRLOPS 960
DB      901 NNEDSDLENSATTTIPIIYPTNILLQDOEDSTLYVSPFKPKTHQVHMYOVRLOPS 960
QY      961 IHDNITPLBAVGVVPOP$E$GPTTHQ$VQ$M$E$PVV$CH$ED$ERL$PDA$E$PC$GAL$FR 1020
DB      961 IHDNITPLBAVGVVPOP$E$GPTTHQ$VQ$M$E$PVV$CH$ED$ERL$PDA$E$PC$GAL$FR 1020
QY      1021 CPVVFROEILVQVIGTLELVGEI$EAS$M$F$LS$SIS$FNS$KH$FHL$YGS$N$A$IAQ$V$M$K 1080
DB      1021 CPVVFROEILVQVIGTLELVGEI$EAS$M$F$LS$SIS$FNS$KH$FHL$YGS$N$A$IAQ$V$M$K 1080
QY      1081 VDVVYERQ$M$LYLVLSGI$GILL$LLIFLYLVYKVPFKRNLK$EM$E$GR$V$P$NCI$P$ED$S 1140
DB      1081 VDVVYERQ$M$LYLVLSGI$GILL$LLIFLYLVYKVPFKRNLK$EM$E$GR$V$P$NCI$P$ED$S 1140
QY      1141 EQLASGOEAGDPGCLKPLH$KDS$E$SG$G$KD 1170
DB      1141 EQLASGOEAGDPGCLKPLH$KDS$E$SG$G$KD 1170

RESULT 6
ABB76377
ID ABB76377 standard; protein; 1170 AA.
XX
AC ABB76377;
XX
DT 22-AUG-2002 (first entry)
XX
DE Lymphocyte function associated antigen-1.
XX
KW Lymphocyte function associated antigen-1; LFA-1; human;
KW alpha/beta protein; ligand binding.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 153..332
FT /label= I_domain
PN MO200231511-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-US032047.
XX

```

PR 12-OCT-2000; 2000US-0239750P.  
 XX (ICOS-) ICOS CORP.  
 PA Stauton DE;  
 PI WPI; 2002-471361/50.  
 DR  
 XX  
 PT Modulating binding interactions between alpha/beta proteins comprising  
 PT allosteric regulatory sites, and a binding partner, by contacting with an  
 CC allosteric effector molecule that interacts with the regulatory site.  
 CC  
 PS Disclosure; Fig 2; 163pp; English.  
 XX  
 CC The present sequence is the protein sequence of lymphocyte function  
 CC associated antigen-1 (LFA-1), which includes an integrin (I) domain. The  
 CC invention provides methods of modulating the binding interaction of a  
 CC first molecule, which is not LFA-1 or an I domain-containing fragment of  
 CC LFA-1, and a binding partner. The first molecule has an alpha/beta domain  
 CC structure comprising an allosteric regulatory site. Modulation of the  
 CC binding interaction involves contacting with an allosteric effector  
 CC molecule that interacts with the regulatory site. In vivo methods are  
 CC expected to alleviate and/or prevent pathological states arising from  
 CC aberrant binding activity. Methods for identifying modulators are also  
 CC provided  
 CC  
 XX Sequence 1170 AA;  
 SQ  
 Query Match 99.9%; Score 6098; DB 5; Length 1170;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 601 VGABSQMIVLSRPPVDMVTLMSPBAIPVHEVBCSYSTSNKMEGNVITTCPIQISLY 660  
 QY 661 PFGQRLVANIITYTLQDGHRTRRRGLEPFGGRHELRNIAVTTSMSCDTSFHPFVCVD 720  
 DB 661 PFGQRLVANIITYTLQDGHRTRRRGLEPFGGRHELRNIAVTTSMSCDTSFHPFVCVD 720  
 QY 721 LISPIVNSLNSWEESTPPDQAOAGKDIPPIIRPSLHSTWEPPEKNGGEKKCAN 780  
 DB 721 LISPIVNSLNSWEESTPPDQAOAGKDIPPIIRPSLHSTWEPPEKNGGEKKCAN 780  
 QY 781 LRVSPSPSRALRLTAPASLVELSLNEEDAWVQDLHPFGGLSFRKYMELKPHSQ 840  
 DB 781 LRVSPSPSRALRLTAPASLVELSLNEEDAWVQDLHPFGGLSFRKYMELKPHSQ 840  
 QY 841 IPVSCBELPEBSRLLSRALSCNVSPIFKAGSVLAQMFTLVNNSWGDVELHANVTC 900  
 DB 841 IPVSCBELPEBSRLLSRALSCNVSPIFKAGSVLAQMFTLVNNSWGDVELHANVTC 900  
 QY 901 NNEDSDLEDNSATTIIPILPINILIDQEDSTLYNSFTFKGKIHOVKMYQVRIOPS 960  
 DB 901 NNEDSDLEDNSATTIIPILPINILIDQEDSTLYNSFTFKGKIHOVKMYQVRIOPS 960  
 QY 961 IHDNIPFLBAVGVGPSPSGPITTHQMSVOMBPVPCHYEDLRLPDPAEPCLPGALFR 1020  
 DB 961 IHDNIPFLBAVGVGPSPSGPITTHQMSVOMBPVPCHYEDLRLPDPAEPCLPGALFR 1020  
 QY 1021 CPVVFROELIVQVIGTELVEIEASSMFSLSLSSISFNSSKPHLYGNSASLAQVVMK 1080  
 DB 1021 CPVVFROELIVQVIGTELVEIEASSMFSLSLSSISFNSSKPHLYGNSASLAQVVMK 1080  
 QY 1081 VDVIYERKQMLTYLYSGIGILLLLIFTVLYKVGFFRRNLKEKMEAGRGVPNGI PAEDS 1140  
 DB 1081 VDVIYERKQMLTYLYSGIGILLLLIFTVLYKVGFFRRNLKEKMEAGRGVPNGI PAEDS 1140  
 QY 1141 BQLASGOEAGDPGCLKPIHEKDSGSGGKD 1170  
 DB 1141 BQLASGOEAGDPGCLKPIHEKDSGSGGKD 1170

RESULT 7  
 ABU05076  
 ID ABU05076 standard; protein, 1170 AA.  
 XX  
 AC ABU05076;  
 XX  
 DT 29-JAN-2003 (first entry)  
 XX  
 DE Human expressed protein tag (BPT) #1742.  
 XX  
 KW Translational profiling; expressed protein tag; BPT; kinase; phosphatase;  
 KW protease; protease inhibitor; transporter; cytoskeletal protein;  
 KW receptor; transcription factor; cancer; MHC;  
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO200278524-A2.  
 XX  
 PD 10-OCT-2002.  
 XX  
 PF 28-MAR-2002; 2002WO-US009671.  
 XX  
 PR 28-MAR-2001; 2001US-0279495P.  
 PR 21-MAY-2001; 2001US-0292544P.  
 PR 08-AUG-2001; 2001US-0310801P.  
 PR 01-OCT-2001; 2001US-0326370P.  
 PR 04-DEC-2001; 2001US-0336780P.  
 PR 20-FEB-2002; 2002US-0358985P.  
 XX  
 PA (ZYCO-) ZYCO INC.

P1 Chicx RM, Tomlinson AJ, Urban RG;  
 XX MPI; 2003-040607/03.  
 XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
 PT cytoskeletal proteins, receptors or transcription factors), useful for  
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
 leukemia.  
 PS Example 2; SEQ ID NO 1742; 134dp; English.  
 XX The invention describes a purified polypeptide, which comprises a  
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
 CC transporter, cytoskeletal protein, receptor or transcription factor. The  
 CC polypeptide is useful as an immunogenic composition for eliciting in a  
 CC mammal an immunogenic response directed against any of the purified  
 CC polypeptide. The purified polypeptide, or the antibody that binds to this  
 CC polypeptide, is useful for treating cancer. The polypeptide is also  
 CC useful for identifying compounds that binds to a naturally processed  
 CC class I or class II MHC-binding polypeptide. The polypeptides and  
 CC polynucleotides are particularly useful for treating or preventing  
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
 CC lymphoma or leukemia. These are also useful for screening agents for  
 CC treating the above mentioned diseases. This sequence represents an  
 CC expressed protein tag (EPT) isolated from human tissue for translational  
 CC profiling. Note: This sequence does not appear in the printed  
 CC specification but was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 1170 AA;  
 SQ

Query Match 99.9%; Score 6098; DB 6; Length 1170;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKDSCTIYMAALISGFFFPAPASSYNDVRGARSFSPRAGRHFGRVLOVANGVIYGA 60  
 DB 1 MKDSCTIYMAALISGFFFPAPASSYNDVRGARSFSPRAGRHFGRVLOVANGVIYGA 60  
 QY 61 PGEKNSGSLVYCCSGTGHCIPVTLRGSNYSKYIGMTLADPMDGSLIADPGISRTCD 120  
 DB 61 PGEKNSGSLVYCCSGTGHCIPVTLRGSNYSKYIGMTLADPMDGSLIADPGISRTCD 120  
 QY 121 QNTTISGLCYLFRONLQGPMLQGRPGFOECIKGNVDLVLFDGSMISLPDEFQKILDFMK 180  
 DB 121 QNTTISGLCYLFRONLQGPMLQGRPGFOECIKGNVDLVLFDGSMISLPDEFQKILDFMK 180  
 QY 181 DVMTKLSTSTYQFAAVQFSTSTYKTFBDFSDYVKRDPALLKHKVHMLLTNTFGAINVY 240  
 DB 181 DVMTKLSTSTYQFAAVQFSTSTYKTFBDFSDYVKRDPALLKHKVHMLLTNTFGAINVY 240  
 QY 241 ATEVFRRELGRPADTKLIIITTOGEANDSGNIDAKIIRIYIGIGHFQTKESQETLH 300  
 DB 241 ATEVFRRELGRPADTKLIIITTOGEANDSGNIDAKIIRIYIGIGHFQTKESQETLH 300  
 QY 301 KFAASKPASEFVKILDTFEKLDLFTLQKTIYVLEGTSKODLTSFMELSSGISADLSR 360  
 DB 301 KFAASKPASEFVKILDTFEKLDLFTLQKTIYVLEGTSKODLTSFMELSSGISADLSR 360  
 QY 361 GHAUVGAVGADWAGFLDLKADLDDDTFIGNEPLTPREVAGYLGITYTWP.PSRQKTSIL 420  
 DB 361 GHAUVGAVGADWAGFLDLKADLDDDTFIGNEPLTPREVAGYLGITYTWP.PSRQKTSIL 420  
 QY 421 ASGARPRYQHMGRVLLFQEPGGGHSQYTIHGTQIGSYFGSELGVVDVDDGRTELLII 480  
 DB 421 ASGARPRYQHMGRVLLFQEPGGGHSQYTIHGTQIGSYFGSELGVVDVDDGRTELLII 480  
 QY 481 GAPLFYGBORGGRVFIYORROLGFEEVESELQDDPYPIGRFGEATLTALTDINGDLVVA 540  
 DB 481 GAPLFYGBORGGRVFIYORROLGFEEVESELQDDPYPIGRFGEATLTALTDINGDLVVA 540  
 QY 541 VGAPLEEGAAVYIFNGRHGSLSPQSPQRIEGTQVLSGIQWFGRSIHGYKDLBGDGLADVA 600  
 DB 541 VGAPLEEGAAVYIFNGRHGSLSPQSPQRIEGTQVLSGIQWFGRSIHGYKDLBGDGLADVA 600

DB 541 VGAPLEEGAAVYIFNGRHGSLSPQSPQRIEGTQVLSGIQWFGRSIHGYKDLBGDGLADVA 600  
 QY 601 VGASQMIYVSSRPVDMTLMSPSPAEIPVHEVECSYSTSNMKKEGVNTTICPOIKSLY 660  
 DB 601 VGASQMIYVSSRPVDMTLMSPSPAEIPVHEVECSYSTSNMKKEGVNTTICPOIKSLY 660  
 QY 661 PQFGRLVANULTYTLQDGRHTRRRGLFPGRRHELRRNIIVTTSMSCTDPSFHPVVCVD 720  
 DB 661 PQFGRLVANULTYTLQDGRHTRRRGLFPGRRHELRRNIIVTTSMSCTDPSFHPVVCVD 720  
 QY 721 LISPINVSLNLSMBEETPRDQRAQKDIPIILRPSLSHETWEIPPEKXCGEDKCEAN 780  
 DB 721 LISPINVSLNLSMBEETPRDQRAQKDIPIILRPSLSHETWEIPPEKXCGEDKCEAN 780  
 QY 781 LRVSFSPARSRLRLTFAASLVELSLSNLEDAVWQLDHPPGISPFKVEMLKPHSQ 840  
 DB 781 LRVSFSPARSRLRLTFAASLVELSLSNLEDAVWQLDHPPGISPFKVEMLKPHSQ 840  
 QY 841 IPVSCEBLPESRRLSRALSCNVSPIFKAGHSVALQMMENTLVNNSWGDVVELHANVTC 900  
 DB 841 IPVSCEBLPESRRLSRALSCNVSPIFKAGHSVALQMMENTLVNNSWGDVVELHANVTC 900  
 QY 901 NMEDSDILEDNSATTIPIIYPINILIQODEDSTLYSFTPKGPKIHQVGMQVRIQPS 960  
 DB 901 NMEDSDILEDNSATTIPIIYPINILIQODEDSTLYSFTPKGPKIHQVGMQVRIQPS 960  
 QY 961 IHDNITPLEAVVGPQPSRGPITHQWSVQMEPPVCHYEDLERLDAEPCLPGLAFR 1020  
 DB 961 IHDNITPLEAVVGPQPSRGPITHQWSVQMEPPVCHYEDLERLDAEPCLPGLAFR 1020  
 QY 1021 CPVFRQELIYOVIGTLELVGEIASMSFSLCSLSISFNSSKHFLYGSNASIAQVVMK 1080  
 DB 1021 CPVFRQELIYOVIGTLELVGEIASMSFSLCSLSISFNSSKHFLYGSNASIAQVVMK 1080  
 QY 1081 VDVIYERQMLYLYLSGIGLLILLIFLYLYKVGFKRNLKEMKMGKGVPIGIPAEIS 1140  
 DB 1081 VDVIYERQMLYLYLSGIGLLILLIFLYLYKVGFKRNLKEMKMGKGVPIGIPAEIS 1140  
 QY 1141 EQLASGOEADPGCLKPLHKDSGSGGKD 1170  
 DB 1141 EQLASGOEADPGCLKPLHKDSGSGGKD 1170

RESULT 8  
 ABU05073  
 ID ABU05073 standard; protein; 1170 AA.  
 AC ABU05073;  
 AC 29-JAN-2003 (first entry)  
 DT 29-JAN-2003 (first entry)  
 XX Human expressed protein tag (EPT) #1739.  
 XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
 KW protease; protease inhibitor; transporter; cytoskeletal protein;  
 KW receptor; transcription factor; cancer; MHC;  
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
 XX Homo sapiens.  
 OS OS  
 PN WO200278524-A2.  
 XX 10-OCT-2002.  
 PD 10-OCT-2002.  
 XX 28-MAR-2002; 2002WO-US009671.  
 XX 28-MAR-2001; 2001US-0279495P.  
 PR 21-MAY-2001; 2001US-0292544P.  
 PR 08-AUG-2001; 2001US-0310801P.  
 PR 01-OCT-2001; 2001US-0326370P.  
 PR 04-DEC-2001; 2001US-0336780P.  
 PR 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCO INC.  
 PA  
 XX Chicx RM, Tomlinson AJ, Urban RG;  
 PI  
 XX WPI; 2003-040607/03.  
 DR  
 XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
 PT cytoskeletal proteins, receptors or transcription factors), useful for  
 PT creating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
 PT leukemia.  
 PS  
 XX Example 2; SEQ ID NO 1739; 134pp; English.  
 CC The invention describes a purified polypeptide, which comprises a  
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
 CC transporter, cytoskeletal protein, receptor or transcription factor. The  
 CC polypeptide is useful as an immunogenic composition for eliciting in a  
 CC mammal an immunogenic response directed against any of the purified  
 CC polypeptide. The purified polypeptide, or the antibody that binds to this  
 CC polypeptide, is useful for treating cancer. The polypeptide is also  
 CC useful for identifying compounds that binds to a naturally processed  
 CC class I or class II MHC-binding polypeptide. The polypeptides and  
 CC polynucleotides are particularly useful for treating or preventing  
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
 CC lymphoma or leukemia. These are also useful for screening agents for  
 CC treating the above mentioned diseases. This sequence represents an  
 CC expressed protein tag (EPT) isolated from human tissue for translational  
 CC profiling. Note: This sequence does not appear in the printed  
 CC specification but was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 CC  
 XX  
 XX Sequence 1170 AA:  
 SQ  
 Query Match 99.9%; Score 6098; DB 6; Length 1170;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 541 VGAPLEEGAGAYIFNGRHGGLSPQSORIGETQVLSGIQWFRGSHIGYKDLBSPGLADVA 600  
 DB 541 VGAPLEEGAGAYIFNGRHGGLSPQSORIGETQVLSGIQWFRGSHIGYKDLBSPGLADVA 600  
 QY 601 VGASQMTIVLSRRVDMVTLMSPSPAEIPVHEVECSYSTSNKKKEGVNITICQIKSLY 660  
 DB 601 VGASQMTIVLSRRVDMVTLMSPSPAEIPVHEVECSYSTSNKKKEGVNITICQIKSLY 660  
 QY 661 POFQGRIVANITYTLQDGHRTRRRGLPFGGRHRLRNIAVTTSMSCDTSFHFPPVCYQD 720  
 DB 661 POFQGRIVANITYTLQDGHRTRRRGLPFGGRHRLRNIAVTTSMSCDTSFHFPPVCYQD 720  
 QY 721 LISPIVNSLMSLWEEBETPPDQAGKDIPILRPSLHSTWTIPPEKNGGEKKCAN 780  
 DB 721 LISPIVNSLMSLWEEBETPPDQAGKDIPILRPSLHSTWTIPPEKNGGEKKCAN 780  
 QY 781 LRVFSFSPARSLALTLTAPASLVELSLSNLEEDAYWQDLHFPFGLSFRKYEMLKPHSQ 840  
 DB 781 LRVFSFSPARSLALTLTAPASLVELSLSNLEEDAYWQDLHFPFGLSFRKYEMLKPHSQ 840  
 QY 841 IPVSCBELPESRLLSRALSCNVSSPIFKAGSHVALQWMENTLVNNSWGDVBLHANTC 900  
 DB 841 IPVSCBELPESRLLSRALSCNVSSPIFKAGSHVALQWMENTLVNNSWGDVBLHANTC 900  
 QY 901 NNEBSDLLEDSATTTIPIILPINILIDQDSDTLVYSFTPKGKXIHQVKMYQVRIOPS 960  
 DB 901 NNEBSDLLEDSATTTIPIILPINILIDQDSDTLVYSFTPKGKXIHQVKMYQVRIOPS 960  
 QY 961 IHDNIPITLNAVGVPOPPSGPITTHQMSVMEPPVPCHEYDRLPLPAAPCPLGALFR 1020  
 DB 961 IHDNIPITLNAVGVPOPPSGPITTHQMSVMEPPVPCHEYDRLPLPAAPCPLGALFR 1020  
 QY 1021 CPVVFROEILVQVIGTLELVEIEASSMFSLCSSLSISFNSSKPHLYGSNASTLAQVVMK 1080  
 DB 1021 CPVVFROEILVQVIGTLELVEIEASSMFSLCSSLSISFNSSKPHLYGSNASTLAQVVMK 1080  
 QY 1081 VDVVYKQMLTYLYLSGIGLLLLIFVLKYKGFGRNLIKEMAEGRGVPNGI PAEDS 1140  
 DB 1081 VDVVYKQMLTYLYLSGIGLLLLIFVLKYKGFGRNLIKEMAEGRGVPNGI PAEDS 1140  
 QY 1141 BQLASGOEAGDPGCLKPLHEKDSGSGGKD 1170  
 DB 1141 BQLASGOEAGDPGCLKPLHEKDSGSGGKD 1170

RESULT 9  
 ABU05071  
 ID ABU05071 standard; protein; 1170 AA.  
 XX  
 AC ABU05071;  
 XX  
 DT 29-JAN-2003 (first entry)  
 XX  
 DE Human expressed protein tag (EPT) #1737.  
 XX  
 KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
 KW protease; transcription inhibitor; transporter; cytoskeletal protein;  
 KW receptor; transcription factor; cancer; MHC;  
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO200278524-A2.  
 XX  
 PD 10-OCT-2002.  
 XX  
 PF 28-MAR-2002; 2002WO-US009671.  
 XX  
 PR 28-MAR-2001; 2001US-0279495P.  
 PR 21-MAY-2001; 2001US-0292544P.  
 PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.  
 PR 04-DEC-2001; 2001US-0336780P.  
 PR 20-FEB-2002; 2002US-0358985P.  
 XX  
 PA (ZYCO-) ZYCOS INC.  
 XX  
 PI Chicx RM, Tomlinson AJ, Urban RG;  
 XX  
 DR WPI; 2003-040607/03.  
 XX  
 PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
 PT cytoskeletal proteins, receptors or transcription factors), useful for  
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
 PT leukemia.  
 XX  
 PS Example 2; SEQ ID NO 1737; 134dp; English.

CC The invention describes a purified polypeptide, which comprises a  
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
 CC transporter, cytoskeletal protein, receptor or transcription factor. The  
 CC polypeptide is useful as an immunogenic composition for eliciting in a  
 CC mammal an immunogenic response directed against any of the purified  
 CC polypeptide. The purified polypeptide, or the antibody that binds to this  
 CC polypeptide, is useful for treating cancer. The polypeptide is also  
 CC useful for identifying compounds that binds to a naturally processed  
 CC class I or class II MHC-binding polypeptide. The polypeptides and  
 CC polynucleotides are particularly useful for treating or preventing  
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
 CC lymphoma or leukemia. These are also useful for screening agents for  
 CC treating the above mentioned diseases. This sequence represents an  
 CC expressed protein tag (EBP) isolated from human tissue for translational  
 CC profiling. Note: This sequence does not appear in the printed  
 CC specification but was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 1170 AA;

Query Match 99.9%; Score 6098; DB 6; Length 1170;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKDSCTIVAMALLSGFFFPASSYNDVVGARSFSPRRGRHGVYLVQNGVYVGA 60  
 DB 1 MKDSCTIVAMALLSGFFFPASSYNDVVGARSFSPRRGRHGVYLVQNGVYVGA 60  
 QY 61 PGEENSTGSLVQCCSGTGHCLPYTLRGSNYSKYLGMTLADPTDGSILACDPGLSRCD 120  
 DB 61 PGEENSTGSLVQCCSGTGHCLPYTLRGSNYSKYLGMTLADPTDGSILACDPGLSRCD 120  
 QY 121 QNTYLSGLCYLFRQNLQSPMLQGRPGFOECIKGNVDLVFLFDGSMSLQPDSEFOKILDFMK 180  
 DB 121 QNTYLSGLCYLFRQNLQSPMLQGRPGFOECIKGNVDLVFLFDGSMSLQPDSEFOKILDFMK 180  
 QY 181 DVMKLSTNTSYQPAVQSTSYKTEFDSYVKRDPALLKHYVMKMLLNTFGAINVY 240  
 DB 181 DVMKLSTNTSYQPAVQSTSYKTEFDSYVKRDPALLKHYVMKMLLNTFGAINVY 240  
 QY 241 ATEVFRREELGARPATKYLIIITDGEATDSGNIDAAKOIIYYIIGIGHFQTKSQETLH 300  
 DB 241 ATEVFRREELGARPATKYLIIITDGEATDSGNIDAAKOIIYYIIGIGHFQTKSQETLH 300  
 QY 301 KFAAKPASEFYKIDTFEKLKDLFTELQKLYIVIEGTSKODLTSFNMELSSSGISADLSR 360  
 DB 301 KFAAKPASEFYKIDTFEKLKDLFTELQKLYIVIEGTSKODLTSFNMELSSSGISADLSR 360  
 QY 361 GHAVVGAIVGADWAGGLDLKADLQDDTFIGNEPITPEVRAGYLGTYTWLPSRKQSTSL 420  
 DB 361 GHAVVGAIVGADWAGGLDLKADLQDDTFIGNEPITPEVRAGYLGTYTWLPSRKQSTSL 420  
 QY 421 ASGAPRYOHMRVULLFQEPGGGHSQVYTHGTOIGSYFGELCGVDVDDGTEBELLI 480  
 DB 421 ASGAPRYOHMRVULLFQEPGGGHSQVYTHGTOIGSYFGELCGVDVDDGTEBELLI 480  
 QY 480 ASGAPRYOHMRVULLFQEPGGGHSQVYTHGTOIGSYFGELCGVDVDDGTEBELLI 480  
 DB 480 ASGAPRYOHMRVULLFQEPGGGHSQVYTHGTOIGSYFGELCGVDVDDGTEBELLI 480

QY 481 GAPLFYGEORGGRVFIYQRRLQGEVESEILQDPCGYLGRFGAITALTDINGDLVDVA 540  
 DB 481 GAPLFYGEORGGRVFIYQRRLQGEVESEILQDPCGYLGRFGAITALTDINGDLVDVA 540  
 QY 541 VGAPLEQAGVYIFNGHGGSLSPQSORIGTOVLSGIQWFGHSIHGVKDLBGDLADVA 600  
 DB 541 VGAPLEQAGVYIFNGHGGSLSPQSORIGTOVLSGIQWFGHSIHGVKDLBGDLADVA 600  
 QY 601 VGASEQWIVLSSRVVMVMTLMSFSPAETPVHRECSYSTSNMKKEVNTITCQIKSLY 660  
 DB 601 VGASEQWIVLSSRVVMVMTLMSFSPAETPVHRECSYSTSNMKKEVNTITCQIKSLY 660  
 QY 661 POFQGRIVANLTYTLQDGHRTTRRGILPQGRHRLRNIAVTTSMSCSTDSPFHPVCVD 720  
 DB 661 POFQGRIVANLTYTLQDGHRTTRRGILPQGRHRLRNIAVTTSMSCSTDSPFHPVCVD 720  
 QY 721 LISPINVSLNPSLMBEETPRDQAGKDIPIILRPSLSEETWEIPERKNGEDKCEAN 780  
 DB 721 LISPINVSLNPSLMBEETPRDQAGKDIPIILRPSLSEETWEIPERKNGEDKCEAN 780  
 QY 781 LRVSFSPARSRALRTAPASLVELSLSNLEBDAYWQDLHPPGISFRKVMELKPHSQ 840  
 DB 781 LRVSFSPARSRALRTAPASLVELSLSNLEBDAYWQDLHPPGISFRKVMELKPHSQ 840  
 QY 841 IPVSCBELPRESRLSRALSCNVSPIFKAGHSVALQMFNTLVNSGDSVVELHANVTC 900  
 DB 841 IPVSCBELPRESRLSRALSCNVSPIFKAGHSVALQMFNTLVNSGDSVVELHANVTC 900  
 QY 901 NNEDSDILENSATTIIPILPINILIQDOEDSTLYVSPFKPKKHQVHMTQVRIOPS 960  
 DB 901 NNEDSDILENSATTIIPILPINILIQDOEDSTLYVSPFKPKKHQVHMTQVRIOPS 960  
 QY 961 IHDNITPLRAVYGVPPSPSGPTTHQMSVQMPVPCHEDELRIPDAAPCLPGALFR 1020  
 DB 961 IHDNITPLRAVYGVPPSPSGPTTHQMSVQMPVPCHEDELRIPDAAPCLPGALFR 1020  
 QY 1021 CPVVFROEILVOVIGLELVEGEIEASSMFSLSLSISFNSSKHFLHYSNASLAQVVMK 1080  
 DB 1021 CPVVFROEILVOVIGLELVEGEIEASSMFSLSLSISFNSSKHFLHYSNASLAQVVMK 1080  
 QY 1081 VDVTYRKQMTLYLVLSTIGGLLILLIFLYLVYGVFFKRNLIKEMEAGRGVNGIPEADS 1140  
 DB 1081 VDVTYRKQMTLYLVLSTIGGLLILLIFLYLVYGVFFKRNLIKEMEAGRGVNGIPEADS 1140  
 QY 1141 EQLASGEAGDPGCLKPLHKKDSBSGGKD 1170  
 DB 1141 EQLASGEAGDPGCLKPLHKKDSBSGGKD 1170

RESULT 10  
 ID ADO43837 standard; protein; 1170 AA.  
 XX  
 AC ADO43837;  
 XX  
 DT 15-JUL-2004 (first entry)  
 XX  
 DE Human lymphocyte function-associated antigen alpha subunit.  
 XX  
 KW Human lymphocyte function-associated antigen; LFA-1; alpha subunit;  
 KW adhesion molecule; cell-cell interaction; inflammation;  
 KW cytotoxic T lymphocyte; CTL-mediated cell lysis; chronic viral hepatitis;  
 KW autoimmune disorder; HIV infection; AIDS;  
 KW acquired immunodeficiency syndrome; CD4+ cell; antibody; Sef1; Tsz/4;  
 KW propeller domain; CD11a; immunogen.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 26..614  
 XX /label = Propeller\_domain  
 PN US2004062765-A1.



XX 01-APR-2004.  
 PD 27-SEP-2002; 2002US-00261164.  
 PF 27-SEP-2002; 2002US-00261164.  
 PR 27-SEP-2002; 2002US-00261164.  
 XX (KAPU/) KAPUSTAY P M.  
 XX (LEWIS/) LEWIS R H.  
 PA (KAPU/) KAPUSTAY P M.  
 PI Kapustay PM, Lewis RH;  
 DR WPI: 2004-294382/27.  
 DR N-PSDB; ADO43839.  
 PT Use of an anti lymphocyte function-associated antigen 1 alpha subunit  
 PT (CD11a) antibody for treating a subject having or at risk of having a  
 PT physiological condition associated with or caused by decreased CD4+ cell  
 PT numbers, e.g. HIV.  
 PS Disclosure; SEQ ID NO 1; 23pp; English.  
 XX The invention relates to treating a subject having or at risk of having a  
 CC physiological condition associated with or caused by decreased CD4+ cell  
 CC numbers, comprising administering an antibody that binds to lymphocyte  
 CC function-associated antigen 1 (LFA-1) alpha subunit (CD11a) in an amount  
 CC greater than 1 mg/kg body weight. LFA-1 is an adhesion molecule involved  
 CC in cell-cell interaction, inflammation, cytotoxic T lymphocyte (CTL)-  
 CC mediated cell lysis and implicated in chronic viral hepatitis, autoimmune  
 CC disorders and HIV infection (AIDS, acquired immunodeficiency syndrome).  
 CC Also included are a composition comprising 100 mg or more S6p1, TS2/4  
 CC antibody (humanized form or its subsequence) and a pharmaceutical  
 CC carrier, a composition comprising 100 mg or more fully human antibody  
 CC having a binding affinity for LFA-1 alpha subunit (or an epitope in LFA-1  
 CC alpha subunit) within about 1-100 of the binding affinity of S6p1 or  
 CC TS2/4 (and a pharmaceutical carrier) and a kit comprising a composition  
 CC above, which is in a single unit dosage form for administration to a  
 CC subject. The antibody inhibits binding of S6p1 or TS2/4 antibody to LFA-1  
 CC alpha subunit, or binds to an epitope to which S6p1 or TS2/4 antibody  
 CC binds, where the epitope comprises an LFA-1 alpha subunit propeller  
 CC domain and is located all or in a part of amino acids 1-57 of the LFA-1  
 CC alpha subunit comprising a sequence of ADO4383. The method is useful for  
 CC increasing CD4+ cell numbers in a subject, for inhibiting or preventing  
 CC decreases in CD4+ cell numbers in a subject, useful for treating a  
 CC subject exposed to HIV or at risk of exposure to HIV. The present  
 CC sequence is the human LFA-1 alpha subunit (CD11a) protein.  
 CC  
 XX Sequence 1170 AA;  
 SQ  
 Query Match 99.9%; Score 6098; DB 8; Length 1170;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 301 KPASKPASEPVKIIDTFEKKLDLFTLEOKKIYVIRGTSKODLTSTNNMELSSSGISADLSR 360  
 DB 301 KPASKPASEPVKIIDTFEKKLDLFTLEOKKIYVIRGTSKODLTSTNNMELSSSGISADLSR 360  
 QY 361 GHAVVGAAGAKDMAGGFIDLKADLDDDFEIGNEPITPEVRAGYGYATYTWLPSPROKSTLL 420  
 DB 361 GHAVVGAAGAKDMAGGFIDLKADLDDDFEIGNEPITPEVRAGYGYATYTWLPSPROKSTLL 420  
 QY 421 ASGAPRYOMGRVLLPQBPQGGHMSQVQTIHGTOIGSYFGGELCGVDVDDQGETELLII 480  
 DB 421 ASGAPRYOMGRVLLPQBPQGGHMSQVQTIHGTOIGSYFGGELCGVDVDDQGETELLII 480  
 QY 481 GAPLPYGGORGRVPTIYRROLGFEVSELOQDDEGYLGRGGEALTALTDINGDGLVYVA 540  
 DB 481 GAPLPYGGORGRVPTIYRROLGFEVSELOQDDEGYLGRGGEALTALTDINGDGLVYVA 540  
 QY 541 VGAPLEEGQAYIYFNGRGGHSPQSQIEGQVLSGIQWGRSIGHVKDLEGDLADVA 600  
 DB 541 VGAPLEEGQAYIYFNGRGGHSPQSQIEGQVLSGIQWGRSIGHVKDLEGDLADVA 600  
 QY 601 VGABEQMIVLSSRPVDMVTLMSPSPAEIPVHEVECSYSTSNKMEGVNITICFOIKSLY 660  
 DB 601 VGABEQMIVLSSRPVDMVTLMSPSPAEIPVHEVECSYSTSNKMEGVNITICFOIKSLY 660  
 QY 661 PQFGRLVANTITLQLDGHRTRRGLPFGGRHRLRNIAVTTSMSCITDSEFHPVCYQD 720  
 DB 661 PQFGRLVANTITLQLDGHRTRRGLPFGGRHRLRNIAVTTSMSCITDSEFHPVCYQD 720  
 QY 721 LISPIVNSLNSLMBEESTPDDORAQGDPIIIRPSLSHTWELPEKNGGEMDKKAN 780  
 DB 721 LISPIVNSLNSLMBEESTPDDORAQGDPIIIRPSLSHTWELPEKNGGEMDKKAN 780  
 QY 781 LRVSFSPASRALRLTAASISVELSLNLEBDAVWQLDLHPPGSLFRKYMELKPHSQ 840  
 DB 781 LRVSFSPASRALRLTAASISVELSLNLEBDAVWQLDLHPPGSLFRKYMELKPHSQ 840  
 QY 841 IPVSCBELPESSRLISRALSCNVSSPIFKAGHSVALQMMFNTLVNSSWGDSEVELHANYTC 900  
 DB 841 IPVSCBELPESSRLISRALSCNVSSPIFKAGHSVALQMMFNTLVNSSWGDSEVELHANYTC 900  
 QY 901 NNEOSDLLENSATITPIIYXINILITODQDSTLYVSFTPKGKIHQVKMYOVRIOPS 960  
 DB 901 NNEOSDLLENSATITPIIYXINILITODQDSTLYVSFTPKGKIHQVKMYOVRIOPS 960  
 QY 961 IHDNIPITLBAVYVQPPSPSGPITTHQWSVOMEPVPCHVEDLRLPPAAEPCLPGALFR 1020  
 DB 961 IHDNIPITLBAVYVQPPSPSGPITTHQWSVOMEPVPCHVEDLRLPPAAEPCLPGALFR 1020  
 QY 1021 CPVVFROEILVQVIGTLELVEIEASSMPSLCSLSISFNSSKHPLYGSNASLAQVVMK 1080  
 DB 1021 CPVVFROEILVQVIGTLELVEIEASSMPSLCSLSISFNSSKHPLYGSNASLAQVVMK 1080  
 QY 1081 VDVIYERQMLLYLISGIGGLLILLLIFIVLYXKGFPRRNKKEKMEAGRGVPGNGIPADS 1140  
 DB 1081 VDVIYERQMLLYLISGIGGLLILLLIFIVLYXKGFPRRNKKEKMEAGRGVPGNGIPADS 1140  
 QY 1141 EQLASGOBAGDPGCLKPLHEKDSSEGGGKD 1170  
 DB 1141 EQLASGOBAGDPGCLKPLHEKDSSEGGGKD 1170  
 RESULT 11  
 ADP12998  
 ID ADP12998 standard; protein; 1170 AA.  
 XX  
 AC ADP12998;  
 DT 12-AUG-2004 (first entry)  
 XX Protein encoding reference mRNA sequence #83.  
 XX transplacental rejection; immune system; rheumatoid arthritis; lupus;  
 KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS.  
 KW



```

XX OS Homo sapiens.
XX MO2004042346-A2.
XX 21-MAY-2004.
XX 24-APR-2003; 2003WO-US012946.
XX 24-APR-2002; 2002US-00131831.
XX 20-DEC-2002; 2002US-00325899.
XX (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M,
XX Rosenberg S;
XX WPI: 2004-400724/37.
XX
XX Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
XX pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
XX rejection, in an individual, comprises detecting the expression level of
XX the genes.
XX
XX Claim 65, SEQ ID NO 3007, 1762bp, English.
XX
XX The present invention relates to diagnosing or monitoring transplant
XX rejection, e.g. cardiac or kidney transplant rejection, in an individual
XX comprising detecting the expression level of one or more genes. The
XX methods, system and kits are useful in diagnosing or monitoring
XX transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
XX islet, lung, bone marrow or stem cell transplant rejection,
XX xenotransplant rejection or mechanical organ replacement rejection, in an
XX individual. The method is also useful in assessing the immune status of
XX an individual. The methods are also useful in diagnosing and monitoring
XX diseases that involve the immune system, e.g. Rheumatoid arthritis,
XX lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
XX viral, bacterial or fungal infection. The present sequence represents a
XX protein encoded by an mRNA sequence of the invention which show altered
XX expression in renal transplantation and expression.
XX
XX Sequence 1170 AA:
XX
Query Match          99.9%; Score 6098; DB 8; Length 1170;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Db 361 GHAVVAVGAKDMAGGFLDLKADLQDDTFIGNEPITPEVBAGYLGYYTWLPSRQKTSLL 420
Qy 421 ASGAPRYQHMGRVLLFQEPQGGHMSQVOTIHGTQISYFGSGLGVVDVQDGETELLII 480
Db 421 ASGAPRYQHMGRVLLFQEPQGGHMSQVOTIHGTQISYFGSGLGVVDVQDGETELLII 480
Qy 481 GAPLFYGBQGRGVFIYQRRQLGFEVSELOQDGPYLGRRGEAITYLTDINGDLVVA 540
Db 481 GAPLFYGBQGRGVFIYQRRQLGFEVSELOQDGPYLGRRGEAITYLTDINGDLVVA 540
Qy 541 VGAPLEEQGANVITNGNHGGLSPQSQRIQSTQVLSGIQWFRGSIHVKOLEGGLDVA 600
Db 541 VGAPLEEQGANVITNGNHGGLSPQSQRIQSTQVLSGIQWFRGSIHVKOLEGGLDVA 600
Qy 541 VGAPLEEQGANVITNGNHGGLSPQSQRIQSTQVLSGIQWFRGSIHVKOLEGGLDVA 600
Db 601 VGASQMIIVLSRRPVDMVMTLMSFPAIPVHEVCYSTSNKKKEGVNITICQIKSLY 660
Qy 601 VGASQMIIVLSRRPVDMVMTLMSFPAIPVHEVCYSTSNKKKEGVNITICQIKSLY 660
Db 601 VGASQMIIVLSRRPVDMVMTLMSFPAIPVHEVCYSTSNKKKEGVNITICQIKSLY 660
Qy 661 POFQRLVANITTYTLQDGHRTRRRLPGGRHRLRNIAVTTSMSCCTDPSFHPVCVQD 720
Db 661 POFQRLVANITTYTLQDGHRTRRRLPGGRHRLRNIAVTTSMSCCTDPSFHPVCVQD 720
Qy 721 LISPINISLMSLEEGTSPDQAGKDIPIILRPSLHBTWEIIPKXGDEKCEAN 780
Db 721 LISPINISLMSLEEGTSPDQAGKDIPIILRPSLHBTWEIIPKXGDEKCEAN 780
Qy 781 LRVSFSPARSALRLTAFASISVLSLSNLEBDAYVWQLDHPFPGSLFRKVEMLKPSHQ 840
Db 781 LRVSFSPARSALRLTAFASISVLSLSNLEBDAYVWQLDHPFPGSLFRKVEMLKPSHQ 840
Qy 841 IPVSCEELPEBSRLLSBALSCNVSSPIFKAGHSVALQMMFNITLVNSWGDSEIHAVTC 900
Db 841 IPVSCEELPEBSRLLSBALSCNVSSPIFKAGHSVALQMMFNITLVNSWGDSEIHAVTC 900
Qy 901 NNEBSDLLENSATITPIIYPIINILQDQEDSTLYSFTPKGKHQVGMVQVRQPS 960
Db 901 NNEBSDLLENSATITPIIYPIINILQDQEDSTLYSFTPKGKHQVGMVQVRQPS 960
Qy 961 IHDNIFTLBAVGVPPPSBGPITTHQMSVQMEPPVCHIEDLERLDAAEPCLPGLAFR 1020
Db 961 IHDNIFTLBAVGVPPPSBGPITTHQMSVQMEPPVCHIEDLERLDAAEPCLPGLAFR 1020
Qy 1021 CPVVFROEIIIVQITIEIVGEIBASSMFSLCSSLSISFNSKXHLXGNSALAQVVMK 1080
Db 1021 CPVVFROEIIIVQITIEIVGEIBASSMFSLCSSLSISFNSKXHLXGNSALAQVVMK 1080
Qy 1081 VDVVYERQMLYLYLSGIGILLILLIFLYLYKVGFFKRNULKEKMEAGRGVPGNIPADS 1140
Db 1081 VDVVYERQMLYLYLSGIGILLILLIFLYLYKVGFFKRNULKEKMEAGRGVPGNIPADS 1140
Qy 1141 EQLASQGBAGDPGCLKPLHEKDESGGAKD 1170
Db 1141 EQLASQGBAGDPGCLKPLHEKDESGGAKD 1170

```

```

RESULT 12
AD039425
ID AD039425 standard; protein: 1170 AA.
AC AD039425;
XX 18-NOV-2004 (first entry)
XX
XX Human myocardial infarction-associated gene derived protein, SEQ ID 1088.
XX Myocardial infarction; detection; single nucleotide polymorphism; SNP;
XX cardiant; gene therapy; human.
XX Homo sapiens.
XX MO2004058052-A2.
XX 15-JUN-2004.

```

XX 22-DEC-2003; 2003WO-US040978.  
 PF  
 XX 20-DEC-2002; 2002US-0434778P.  
 PR 10-MAR-2003; 2003US-0453135P.  
 PR 30-APR-2003; 2003US-0466412P.  
 PR 23-SEP-2003; 2003US-0504955P.  
 XX  
 PA (APPL-) APPLERA CORP.  
 XX  
 XX Cargill M, Devlin J, Iakoubova O;  
 XX MPI: 2004-533949/51.  
 DR N-PSDB; AD038597.  
 PT Identifying an individual who has an altered risk for developing  
 PT myocardial infarction by detecting a single nucleotide polymorphism in  
 PT the individual's nucleic acids.  
 XX  
 PS Claim 10; SEQ ID NO 1088; 145bp; English.  
 CC The invention relates to a novel method for identifying an individual who  
 CC has an altered risk for developing myocardial infarction. The method  
 CC comprises detecting a single nucleotide polymorphism (SNP) in any one of  
 CC the nucleotide sequences given in the specification in the individual's  
 CC nucleic acids, where the presence of the SNP is correlated with an  
 CC altered risk for myocardial infarction in the individual. The invention  
 CC further comprises: an isolated nucleic acid molecule comprising at least  
 CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in  
 CC the specification or its complement and encoding any one of the amino  
 CC acid sequences given in the specification; an isolated polypeptide  
 CC comprising an amino acid sequence given in the specification; an antibody  
 CC that specifically binds to the polypeptide or its antigen-binding  
 CC fragment; an amplified polynucleotide containing an SNP given in the  
 CC specification and which is between about 16 and 1000 nucleotides in  
 CC length; a kit for detecting an SNP in a nucleic acid, comprising the  
 CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a  
 CC nucleic acid molecule; a method of detecting a variant polypeptide; and a  
 CC method for identifying an agent useful in treating or preventing  
 CC myocardial infarction. The novel detection method has cardiant activity.  
 CC The nucleic acids of the invention may be used in gene therapy. The  
 CC method is useful in identifying an individual who has an increased or  
 CC decreased risk for developing myocardial infarction and for preparing a  
 CC composition for treating or preventing myocardial infarction. This  
 CC sequence represents the protein of a human myocardial infarction-  
 CC associated gene containing one or more SNP's of the invention. Note: This  
 CC sequence was not shown in the specification. The sequence has come from  
 CC an electronic sequence listing downloaded from the WIPO website.  
 XX  
 SQ Sequence 1170 AA;  
 Query Match 99.9%; Score 6098; DB 8; Length 1170;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 241 ATEVERBELGARPDATKVLIIITDGEATDSGNIDAKDIIIRYIGIGKHFOTKESQETLH 300  
 QY 301 KPASKPASEFYKILDTFEKFKDLTELOKTIYVIGTSKQULTSPNNELSSSGISADLSR 360  
 Db 301 KPASKPASEFYKILDTFEKFKDLTELOKTIYVIGTSKQULTSPNNELSSSGISADLSR 360  
 QY 361 GHAVVGAAGAKMDAGGFDLAKADLODDPFIGNEPITPEVRAGYGYATYTMPSROKSTL 420  
 Db 361 GHAVVGAAGAKMDAGGFDLAKADLODDPFIGNEPITPEVRAGYGYATYTMPSROKSTL 420  
 QY 421 ASGAPRYOMGRVLLFQEPQGGHMSQVQTIHGTOIGSPFGELCGVDVDDGETELLII 480  
 Db 421 ASGAPRYOMGRVLLFQEPQGGHMSQVQTIHGTOIGSPFGELCGVDVDDGETELLII 480  
 QY 481 GAPIFYGEORGRVFIYORROLGFEVSELQDDPGYPIGRGEAITALTDINGDLVDVA 540  
 Db 481 GAPIFYGEORGRVFIYORROLGFEVSELQDDPGYPIGRGEAITALTDINGDLVDVA 540  
 QY 541 VGAPLEEGAVYIRNGRHGGLSPQSORIESTOYLSGIQWFGRSIHVKDLEGDLADVA 600  
 Db 541 VGAPLEEGAVYIRNGRHGGLSPQSORIESTOYLSGIQWFGRSIHVKDLEGDLADVA 600  
 QY 601 VGASQMTVLSRRPVDMVTLMSPPAEIPVHEVCSYSTGNKKEGVNITICFOIKSLY 660  
 Db 601 VGASQMTVLSRRPVDMVTLMSPPAEIPVHEVCSYSTGNKKEGVNITICFOIKSLY 660  
 QY 661 POFQRLVANTTYTLQDGHRTRRRLPPGGRHRLRNIAVTTSMCTDFSHPFPVQVD 720  
 Db 661 POFQRLVANTTYTLQDGHRTRRRLPPGGRHRLRNIAVTTSMCTDFSHPFPVQVD 720  
 QY 721 LISPIVNSLNSLWEEBETPDQAOQGDIPILRPSLHSTWETIPEKNGGEKKCAN 780  
 Db 721 LISPIVNSLNSLWEEBETPDQAOQGDIPILRPSLHSTWETIPEKNGGEKKCAN 780  
 QY 781 LRVSFSPARSLRLTAASLVELSLNLEBDAYWQDLAPPGLSFRKYMELKPSQ 840  
 Db 781 LRVSFSPARSLRLTAASLVELSLNLEBDAYWQDLAPPGLSFRKYMELKPSQ 840  
 QY 841 IPVSCBELPEBSRLLSRALSCNVSSPIFKAGSHVALQMMFNTLVNNSWGDVBLHANTC 900  
 Db 841 IPVSCBELPEBSRLLSRALSCNVSSPIFKAGSHVALQMMFNTLVNNSWGDVBLHANTC 900  
 QY 901 NNEBSDLLEDSATTIPIILPINILQDDSDTLVYSFTKGGKIHQVKMYOVRQPS 960  
 Db 901 NNEBSDLLEDSATTIPIILPINILQDDSDTLVYSFTKGGKIHQVKMYOVRQPS 960  
 QY 961 IHDNIIPTLEAVGVPOPSPSGPITTHQMSVOMEPVPCHYEDELRLPDAAPCLPGALFR 1020  
 Db 961 IHDNIIPTLEAVGVPOPSPSGPITTHQMSVOMEPVPCHYEDELRLPDAAPCLPGALFR 1020  
 QY 1021 CPVVFROEILVOVITGELVGEIEASSMFSICSSLSISFNSSKHFHLYGSNASTLAQVVMK 1080  
 Db 1021 CPVVFROEILVOVITGELVGEIEASSMFSICSSLSISFNSSKHFHLYGSNASTLAQVVMK 1080  
 QY 1081 VDVIYKEMLYLYLSGIGLLLLLIIFTVLKYKGFGRNKKEMAGRGVPGNIPADS 1140  
 Db 1081 VDVIYKEMLYLYLSGIGLLLLLIIFTVLKYKGFGRNKKEMAGRGVPGNIPADS 1140  
 QY 1141 BOLASGEAGDPGLCKPLHEKDSRSGGKD 1170  
 Db 1141 BOLASGEAGDPGLCKPLHEKDSRSGGKD 1170  
 RESULT 13  
 AAR05782  
 ID AAR05782 standard; protein, 1170 AA.  
 XX  
 AC AAR05782;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 09-JAN-2003 (revised)  
 DT 23-AUG-1990 (first entry)  
 XX

DE	LFA-1 alpha subunit.	
XX	Lymphocyte function associated antigen; inflammation; metastasis.	
KW		
XX	Homo sapiens.	
OS		
XX		
PH	Key	Location/Qualifiers
FT	Peptide	1..25
FT		/label= sig_peptide
FT	Domain	26..1088
FT		/label= extracellular_domain
FT	Modified-site	65..67
FT		/label= N-glycosylation_site
FT	Modified-site	89..91
FT		/label= N-glycosylation_site
FT	Peptide	118..132
FT		/label= tryptic_fragment
FT	Modified-site	188..190
FT		/label= N-glycosylation_site
FT	Peptide	226..237
FT		/label= tryptic_fragment
FT	Peptide	282..288
FT		/label= tryptic_fragment
FT	Peptide	433..441
FT		/label= tryptic_fragment
FT	Peptide	521..531
FT		/label= tryptic_fragment
FT	Peptide	569..582
FT		/label= tryptic_fragment
FT	Peptide	590..604
FT		/label= tryptic_fragment
FT	Modified-site	649..651
FT		/label= N-glycosylation_site
FT	Modified-site	670..672
FT		/label= N-glycosylation_site
FT	Modified-site	726..728
FT		/label= N-glycosylation_site
FT	Modified-site	730..732
FT		/label= N-glycosylation_site
FT	Peptide	831..844
FT		/label= tryptic_fragment
FT	Modified-site	862..864
FT		/label= N-glycosylation_site
FT	Modified-site	885..887
FT		/label= N-glycosylation_site
FT	Modified-site	897..899
FT		/label= N-glycosylation_site
FT	Peptide	957..974
FT		/label= tryptic_fragment
FT	Modified-site	1060..1062
FT		/label= N-glycosylation_site
FT	Modified-site	1071..1073
FT		/label= N-glycosylation_site
FT	Domain	1089..1117
FT		/label= transmembrane_domain
FT	Region	1118..1170
FT		/label= cytoplasmic_tail
FT	Modified-site	1140
FT		/label= serine_phosphorylation_site
FT	Modified-site	1145
FT		/label= serine_phosphorylation_site
FT	Modified-site	1163
FT		/label= serine_phosphorylation_site
FT	Modified-site	1165
FT		/label= serine_phosphorylation_site
XX		
PN	EP362526-A.	
XX		
PD	11-APR-1990.	
XX		
DP	17-AUG-1989;	89EP-00115160.
XX		
PR	23-AUG-1988;	88US-00235227.

Query	Best Local Match	Similarity	Score	Pred.	No. of Matches	Conservative	Mismatches	Indels	Gaps
09-MAR-1989;	89US-00321017.								
XX	(DAND )	DANA FARBER CANCER INST INC.							
PA	(DANA )	DANFOSS A/S.							
PA	(DAND )	DANA FARBER CANCER INST INC.							
XX	Springer TA,	Lateon R,							
XX	WP1; 1990-108985/15.								
DR	N-PSDB; AAQ03842.								
XX	Pure alpha subunit of lymphocyte function associated antigen - and								
PT	encoding DNA sequences, useful e.g. for suppressing inflammation or								
PT	metastasis.								
XX	Disclosure; Fig 3; 27pp; English.								
XX	The alpha-subunit (a-SU) can bind to ICAM-1 (or other natural ligands) on								
CC	the surface of cells, and can associate with the beta-SU to form a								
CC	heterodimer (also able to bind to ICAM-1). a-SU, and its derivs., are								
CC	useful in suppressing inflammation, metastasis and growth of a-SU								
CC	expressing tumour cells and is used in the treatment of viral infections.								
CC	The pref. dose is 1 pg - 10 mg/kg. (updated on 09-JUN-2003 to add missing								
CC	OS field.) (updated on 25-MAR-2003 to correct PA field.) (updated on 25-								
CC	MAR-2003 to correct PI field.)								
XX	Sequence 1170 AA;								
XX	Query Match	99.4%;	Score 6072;	DB 2;	Length 1170;				
XX	Best Local Similarity	99.6%;	Pred. No. 0;						
XX	Matches 1165;	Conservative 0;	Mismatches 5;	Indels 0;	Gaps 0;				
QY	1	MKOSCIIVMMALISGFFFPAPASSYVLDYRGARSFSPRAGRHFGYRVLVQVNGVIYGA	60						
DB	1	MKOSCIIVMMALISGFFFPAPASSYVLDYRGARSFSPRAGRHFGYRVLVQVNGVIYGA	60						
QY	61	PGBSNTSGSLYQCCSGTGHCPLPYTLRGSNYSKYLGMTLATDPTDGSIIACDGLSRTCD	120						
DB	61	PGBSNTSGSLYQCCSGTGHCPLPYTLRGSNYSKYLGMTLATDPTDGSIIACDGLSRTCD	120						
QY	121	QNTYLSGLCYLFRONTLQGMLOGRPGQECIKGNVDLVFLPDSMSLQDPEPKIIDPMK	180						
DB	121	QNTYLSGLCYLFRONTLQGMLOGRPGQECIKGNVDLVFLPDSMSLQDPEPKIIDPMK	180						
QY	181	DVMKLSNTSYQFAAVQFSTSYKTEPFPDSYVYRKDPDALKKVKKMLLTNTFGAINTY	240						
DB	181	DVMKLSNTSYQFAAVQFSTSYKTEPFPDSYVYRKDPDALKKVKKMLLTNTFGAINTY	240						
QY	241	ATEVEFREELGAPDPAIVLLIITDGEATDSGNIDAADIIIRYIIIGIKHFQYKSEQETLL	300						
DB	241	ATEVEFREELGAPDPAIVLLIITDGEATDSGNIDAADIIIRYIIIGIKHFQYKSEQETLL	300						
QY	301	KFASKKASSEVVKIIDTPEKIKDLFTBLQKTIYIEGTSKODLTSFMWELSSSGISADLSR	360						
DB	301	KFASKKASSEVVKIIDTPEKIKDLFTBLQKTIYIEGTSKODLTSFMWELSSSGISADLSR	360						
QY	361	GHAIVGAVGAKDMAGGFLDKADLQDDTFIGNEPILPEVAGYGLGYTVWLPEROKTSLI	420						
DB	361	GHAIVGAVGAKDMAGGFLDKADLQDDTFIGNEPILPEVAGYGLGYTVWLPEROKTSLI	420						
QY	421	ASGAPRYQHMGRVLLFOEPQGGHWSQVOTIHGTQIGSYFGSELGCVDVDODDETELLI	480						
DB	421	AMGAPRYQHMGRVLLFOEPQGGHWSQVOTIHGTQIGSYFGSELGCVDVDODDETELLI	480						
QY	481	GAPLFYGEORGRVFIYQRPQLGFEYVSEIQDPPGLRFGGALITALDINDGVLVDYA	540						
DB	481	GAPLFYGEORGRVFIYQRPQLGFEYVSEIQDPPGLRFGGALITALDINDGVLVDYA	540						
QY	541	VGAPLEEGQAVYIFNGHGGSLPQSPQRJEGTGVLSGIQWFGSHGVGVDLBEDGLADV	600						
DB	541	VGAPLEEGQAVYIFNGHGGSLPQSPQRJEGTGVLSGIQWFGSHGVGVDLBEDGLADV	600						
QY	601	VGASSQMIIVLSSRPVDMVTLMSFSPALIPVHVESGYSYNNMKKGAVNTTICFOIKSLY	660						

```

Db 601 VGABQMTVLSSRPVVDVMTLMSFSPALPHEVCSTSTSKMKGAVNTTICFOIKSLY 660
Qy 661 POFQRLVAVNTLYTLQDGHRTTRRGGLPGGHELRNIAVTTSTSCDPSFHPVQVOD 720
Db 661 POFQRLVAVNTLYTLQDGHRTTRRGGLPGGHELRNIAVTTSTSCDPSFHPVQVOD 720
Qy 721 LISPIVNSLNFSLMEEGTPRQROQKDIPIILRSLHSEIWEIPEKNCCEKCCAN 780
Db 721 LISPIVNSLNFSLMEEGTPRQROQKDIPIILRSLHSEIWEIPEKNCCEKCCAN 780
Qy 781 LRVSPARSRLRLTAFASSLSEVLSNLJEDATWVOLDLHPFGSLFRKXEMLKPSQ 840
Db 781 LRVSPARSRLRLTAFASSLSEVLSNLJEDATWVOLDLHPFGSLFRKXEMLKPSQ 840
Qy 841 IPVSCBEPBESRLSRALSCNVSPIFKAGHSVALQWMTLVNNSWGDSEIHLANYTC 900
Db 841 IPVSCBEPBESRLSRALSCNVSPIFKAGHSVALQWMTLVNNSWGDSEIHLANYTC 900
Qy 901 NNHBDLLJEDNSATITIPILPINILIDQEDSTLYSFTPKGPKIHQVMYQVRIQPS 960
Db 901 NNHBDLLJEDNSATITIPILPINILIDQEDSTLYSFTPKGPKIHQVMYQVRIQPS 960
Qy 961 IHDHNIPTLEAVGVPOPSEGPITHQMSVQMEPPVPCHEBDLERLPAABPCLPALFR 1020
Db 961 IHDHNIPTLEAVGVPOPSEGPITHQMSVQMEPPVPCHEBDLERLPAABPCLPALFR 1020
Qy 1021 CPVVRQELIVQVIGTLEIVGEIEASSMFSLCSSISIFNSKPHLYGSNASTLAQVMK 1080
Db 1021 CPVVRQELIVQVIGTLEIVGEIEASSMFSLCSSISIFNSKPHLYGSNASTLAQVMK 1080
Qy 1081 VDVIYKQMLYLYVLSGIGGLILLIFLYLVKVGFPKRNLEKXMEAGRGVNGIPADS 1140
Db 1081 VDVIYKQMLYLYVLSGIGGLILLIFLYLVKVGFPKRNLEKXMEAGRGVNGIPADS 1140
Qy 1141 EQLASGOAGDPGCCPLHKKDSESGKD 1170
Db 1141 EQLASGOAGDPGCCPLHKKDSESGKD 1170

RESULT 14
ADQ39423 standard; protein; 1223 AA.
AC ADQ39423;
DT 18-NOV-2004 (first entry)
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1086.
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
OS Homo sapiens.
PN WO2004058052-A2.
PD 15-JUL-2004.
PE 22-DEC-2003; 2003WO-US040978.
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-045135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
PA (APPL-) APPLERA CORP.
PI Cargill M, Devlin J, Iakoubova O;
DR WPI, 2004-533949/51.
DR N-PsDB; ADQ38595.
XX

```

```

PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
PS Claim 10; SEQ ID NO 1086; 145pp; English.
XX
XX The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC sequence represents the protein of a human myocardial infarction-
CC associated gene containing one or more SNPs of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.
XX
XX Sequence 1223 AA:
Qy Query Match 99.3%; Score 6061.5; DB 8; Length 1223;
Db Best Local Similarity 95.6%; Pred. No. 0;
Db Matches 1169; Conservative 0; Mismatches 1; Indels 53; Gaps 1;

1 MKDSCITVMAMALLSGFFFPAPASSYNDVARGASFPSPRAGRHYGVLOVNGVYIGA 60
1 MKDSCITVMAMALLSGFFFPAPASSYNDVARGASFPSPRAGRHYGVLOVNGVYIGA 60
Qy 61 PEGNSTGSLYQCCSGTGCHLPTVLIRGSNTYSKYLGMTLATDPTDGSILACDPSLRCD 120
Db 61 PEGNSTGSLYQCCSGTGCHLPTVLIRGSNTYSKYLGMTLATDPTDGSILACDPSLRCD 120
Qy 121 QNTYLSGLCYLFRONTLOGPMLQGRPGQECTKGNVDLVFLFDGSMISQPDFQKILDPMK 180
Db 121 QNTYLSGLCYLFRONTLOGPMLQGRPGQECTKGNVDLVFLFDGSMISQPDFQKILDPMK 180
Qy 181 DVMKKLSNTSYQFAAVQFSTSYKTEPDSVDYRKDDPALKHVMHLLNTNGAINVY 240
Db 181 DVMKKLSNTSYQFAAVQFSTSYKTEPDSVDYRKDDPALKHVMHLLNTNGAINVY 240
Qy 241 ATEVFRBELGARPDATVLIITDGEATDSGNIDAADIIIRYIIGIKHFPQKESQETLH 300
Db 241 ATEVFRBELGARPDATVLIITDGEATDSGNIDAADIIIRYIIGIKHFPQKESQETLH 300
Qy 301 KFAASKPASEFYKIIDTEBKLKDLFTBLQKIIYIEGTSKODLISFNNELSSGSIADLSR 360
Db 301 KFAASKPASEFYKIIDTEBKLKDLFTBLQKIIYIEGTSKODLISFNNELSSGSIADLSR 360
Qy 361 GHAVVAVGAKDWAAGFLLDKADLQDDTPIGNEPLFEVARGVLYGYVTWMLPSQKSTLL 420
Db 361 GHAVVAVGAKDWAAGFLLDKADLQDDTPIGNEPLFEVARGVLYGYVTWMLPSQKSTLL 420
Qy 421 ASGAPRYOHMGRLVLLFQEPQGGHMSQVQTHGTQISYFGELCGVDVDDQGETELLII 480
Db 421 ASGAPRYOHMGRLVLLFQEPQGGHMSQVQTHGTQISYFGELCGVDVDDQGETELLII 480
Qy 481 GAPLFYGEQGRGRVFIYQRRQLGRBEVSELOGDPRGYLGRGRGAITLTLTDINGGLYDVA 540

```

```

Db      481  GAPLFYGGQGRGVFIYQRQLGFEVEVELQGDPEYPIGRFGEATALTLDINGGLVDVA 540
Qy      541  VGAPLEEGGAYYIFNGRHGSLSPQPSORIIEGQVLSGIQWFGRSIHGKDLDEGLADVA 600
Db      541  VGAPLEEGGAYYIFNGRHGSLSPQPSORIIEGQVLSGIQWFGRSIHGKDLDEGLADVA 600
Qy      601  VGASQMIVLSSRPVDMVTLMSPAPAI PVHEVECSYSTSNKKEGVNITICQIKSLY 660
Db      601  VGASQMIVLSSRPVDMVTLMSPAPAI PVHEVECSYSTSNKKEGVNITICQIKSLI 660
Qy      661  PFGQRLVANTITLTQLDGHTRRGFLPGGRHELRRIAVTTSCTDSFHHPPVCQD 720
Db      661  PFGQRLVANTITLTQLDGHTRRGFLPGGRHELRRIAVTTSCTDSFHHPPVCQD 720
Qy      721  LISPIVSLNFWLMBEESTPRDQROGKDIPIILRSLHSFTWELPEKNGGDKKCGAN 780
Db      721  LISPIVSLNFWLMBEESTPRDQROGKDIPIILRSLHSFTWELPEKNGGDKKCGAN 780
Qy      781  LRVSPSPARBALRLTAPASISVLSLSNLEDAWVQDLHPFGSLFRKVEMLKPHSQ 840
Db      781  LRVSPSPARBALRLTAPASISVLSLSNLEDAWVQDLHPFGSLFRKVEMLKPHSQ 840
Qy      841  IPVCEELPEESRLISRLSCNVSSPIFKAGHSVALQWMENTLYNSWGSVEIHLANTC 900
Db      841  IPVCEELPEESRLISRLSCNVSSPIFKAGHSVALQWMENTLYNSWGSVEIHLANTC 900
Qy      901  NNEBSDLEDNSATTIPIILYPINILIDQEDSTLYSFTFKGPKIHQVKHMYQ----- 954
Db      901  NNEBSDLEDNSATTIPIILYPINILIDQEDSTLYSFTFKGPKIHQVKHMYQGVGLV 960
Qy      955  -----VRIPSIDHNIP 967
Db      961  EMQTSKQILCRPAGDAEHTVGAQEGELPCPWGSEAFARDNI RAGPCRVRIQPSIHDNIP 1020
Qy      968  TLEAVNGVPQPPSPGPITHQWSVQMEPPVPCHEYLELPLDAABCLFGALFRCPVPRQ 1027
Db      1021  TLEAVNGVPQPPSPGPITHQWSVQMEPPVPCHEYLELPLDAABCLFGALFRCPVPRQ 1080
Qy      1028  EILVQVIGTLELVGEIEASMFSLCSSLSISFNSSKPHLYGSNLSAQVVMKVDVYVK 1087
Db      1081  EILVQVIGTLELVGEIEASMFSLCSSLSISFNSSKPHLYGSNLSAQVVMKVDVYVK 1140
Qy      1088  QMLTYLVLSGIGLILLILFIVLYKVGFPRNLKEKMEAGRGVPGNGIPADBSQLASGQ 1147
Db      1141  QMLTYLVLSGIGLILLILFIVLYKVGFPRNLKEKMEAGRGVPGNGIPADBSQLASGQ 1200
Qy      1148  EAGDPGCLKPLHEKDSBSGGKD 1170
Db      1201  EAGDPGCLKPLHEKDSBSGGKD 1223

RESULT 15
ABU05070
ID      ABU05070 standard; protein; 1223 AA.
XX      ABU05070;
AC      29-JAN-2003 (first entry)
DE      Human expressed protein tag (EPT) #1736.
XX      Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW      protease; protease inhibitor; transporter; cytoskeletal protein;
KW      receptor; transcription factor; cancer; MHC;
KW      major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW      adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX      Homo sapiens.
OS      MO200278524-A2.
PN      10-OCT-2002.
PD

```

```

XX      28-MAR-2002; 2002WO-US009671.
PF      28-MAR-2001; 2001US-0279495P.
XX      21-MAY-2001; 2001US-0292544P.
PR      08-AUG-2001; 2001US-0310801P.
PR      01-OCT-2001; 2001US-0326370P.
PR      04-DEC-2001; 2001US-0336780P.
PR      20-FEB-2002; 2002US-0358985P.
XX      (ZYCO-) ZYCOS INC.
PA      Chicz RM, Tomlinson AJ, Urban RG;
PI      WPI; 2003-040607/03.
XX      New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT      cytoskeletal proteins, receptors or transcription factors), useful for
PT      treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT      leukemia.
XX      Example 2; SEQ ID NO 1736; 134pp; English.
PS      The invention describes a purified polypeptide, which comprises a
XX      fragment of a kinase, phosphatase, protease, protease inhibitor,
XX      transporter, cytoskeletal protein, receptor or transcription factor. The
XX      polypeptide is useful as an immunogenic composition for eliciting in a
XX      mammal an immunogenic response directed against any of the purified
XX      polypeptide. The purified polypeptide, or the antibody that binds to this
XX      polypeptide, is useful for treating cancer. The polypeptide is also
XX      useful for identifying compounds that binds to a naturally processed
XX      class I or class II MHC-binding polypeptide. The polypeptides and
XX      polynucleotides are particularly useful for treating or preventing
XX      myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX      lymphoma or leukaemia. These are also useful for screening agents for
XX      treating the above mentioned diseases. This sequence represents an
XX      expressed protein tag (EPT) isolated from human tissue for translational
XX      profiling. Note: This sequence does not appear in the printed
XX      specification but was obtained in electronic format directly from WIPO at
XX      ftp.wipo.int/pub/published_pct_sequences
SQ      Sequence 1223 AA;
Qy      1 MKDSCTVMAMALLISGFFFPAPASSTYLDVYGARSFSPAPAGHFGYRVLQVANGVIVGA 60
Db      1 MKDSCTVMAMALLISGFFFPAPASSTYLDVYGARSFSPAPAGHFGYRVLQVANGVIVGA 60
Qy      61 PGBGNSGSLYQCOOSGTHCLPVTLRGNSNTSYKLGWTLATDPTDGSIIACDGLSTCD 120
Db      61 PGBGNSGSLYQCOOSGTHCLPVTLRGNSNTSYKLGWTLATDPTDGSIIACDGLSTCD 120
Qy      121 QNTYLSGLCYLFRQNLQGPMLQGRPGFOECIKGNVDLVFLFDGSMSTLQDPFQKILDFMK 180
Db      121 QNTYLSGLCYLFRQNLQGPMLQGRPGFOECIKGNVDLVFLFDGSMSTLQDPFQKILDFMK 180
Qy      181 DVNKKLSNTSYQPAVQSTSYTEBDFSDYVRKQPDALLKVKVKNMLLTNTFGAINVY 240
Db      181 DVNKKLSNTSYQPAVQSTSYTEBDFSDYVRKQPDALLKVKVKNMLLTNTFGAINVY 240
Qy      241 ATVEPRELQARPDATVLIITIDGAEVDSGNIDAKDIIRYITIGKHPQTESQOETLH 300
Db      241 ATVEPRELQARPDATVLIITIDGAEVDSGNIDAKDIIRYITIGKHPQTESQOETLH 300
Qy      301 KFASKPASEFVKILDTFEKLDLFTTELQKKIYVIEGTSKODLTSFMMELSSSGISADLSR 360
Db      301 KFASKPASEFVKILDTFEKLDLFTTELQKKIYVIEGTSKODLTSFMMELSSSGISADLSR 360
Qy      361 GHAVVGAAGKADWAGFLDKADLQDDTFIGNBPLTPEVAVAGLYGTVTWLPSRQKTSLL 420

```

Db 361 GHAUVAVAGAKDMAGGFLDLKADLODDPFIENEPLTPEVRAGVIGYVTWLPSPQKTSLL 420  
QY 421 ASQAPRYOMGVRVLLFQEPQGGGHSQVTTIHGTQIGSYFGGRLCGVDYDQGETELLII 480  
Db 421 ASQAPRYOMGVRVLLFQEPQGGGHSQVTTIHGTQIGSYFGGRLCGVDYDQGETELLII 480  
QY 481 GAPLFYGEORGRVFTYQRRQLGFEBSLQDPPGYPLGRFGEAITALTIDINGDLADVA 540  
Db 481 GAPLFYGEORGRVFTYQRRQLGFEBSLQDPPGYPLGRFGEAITALTIDINGDLADVA 540  
QY 541 VGAPLEEOGAVYIFNGRHGGLSPQSPQRIEGTVLSGIOWFGRSIHGVNDELDGLADVA 600  
Db 541 VGAPLEEOGAVYIFNGRHGGLSPQSPQRIEGTVLSGIOWFGRSIHGVNDELDGLADVA 600  
QY 601 VQAESOMIVLSRPVVDVMTLMSFSPAELPHEVECSYSTSNMKEGVNITICFOIKSLY 660  
Db 601 VQAESOMIVLSRPVVDVMTLMSFSPAELPHEVECSYSTSNMKEGVNITICFOIKSLY 660  
QY 661 PQFQRLVANLTYTLODGHRTRRRGLFPGGRHBLRRNIAVTTSMSCTDSEFHPVCVD 720  
Db 661 PQFQRLVANLTYTLODGHRTRRRGLFPGGRHBLRRNIAVTTSMSCTDSEFHPVCVD 720  
QY 721 LISPINVSLNFSLWEEBGTPRDQAGKDIPIILRPSLHSETWEIPEKNCGEDKCEAN 780  
Db 721 LISPINVSLNFSLWEEBGTPRDQAGKDIPIILRPSLHSETWEIPEKNCGEDKCEAN 780  
QY 781 LRVSFSPASRALRLTAFASLSVEISLSNLEEDAYWQDLHFPGLSFRKYTEMLKPHSQ 840  
Db 781 LRVSFSPASRALRLTAFASLSVEISLSNLEEDAYWQDLHFPGLSFRKYTEMLKPHSQ 840  
QY 841 IPVSCBELPEBSRLSRLASCNVSSPIFAGHSVALQMMFNTLVNNSWGDVTELANVTC 900  
Db 841 IPVSCBELPEBSRLSRLASCNVSSPIFAGHSVALQMMFNTLVNNSWGDVTELANVTC 900  
QY 901 NNEDSDLEEDNSATTIIPILYPINILIQOEDSTLYVSFTPKGPKIHQVGHMYQ----- 954  
Db 901 NNEDSDLEEDNSATTIIPILYPINILIQOEDSTLYVSFTPKGPKIHQVGHMYQ----- 954  
QY 955 -----VRIQPSIHQHNIP 967  
Db 961 EMQTSKQILCRPAGDAEHTVGAQEGELPCPMGVSEAFRDNIAPGCRVRIQPSIHQHNIP 1020  
QY 966 TLBAVVGVPQPSSEGPITHQMSVOMEPPVCHYEDLERLDDAABPCLRGALFRCVVRQ 1027  
Db 1021 TLBAVVGVPQPSSEGPITHQMSVOMEPPVCHYEDLERLDDAABPCLRGALFRCVVRQ 1027  
QY 1028 EILVVOVIGTLBLVGEIEASSMFLSCSLISFNSSKHFLYGSNASLAQVWKVDVYEX 1087  
Db 1081 EILVVOVIGTLBLVGEIEASSMFLSCSLISFNSSKHFLYGSNASLAQVWKVDVYEX 1087  
QY 1088 QMLYLYVLSGIGLLLLLIIFVLVYKVGFFKKNLKEKMEAGRGVNGIIPAEDESQLASQ 1147  
Db 1141 QMLYLYVLSGIGLLLLLIIFVLVYKVGFFKKNLKEKMEAGRGVNGIIPAEDESQLASQ 1147  
QY 1148 EADDPGCLKPLHEKSESGGKD 1170  
Db 1201 EADDPGCLKPLHEKSESGGKD 1223

Search completed: August 29, 2005, 19:21:49  
Job time : 107 secs

***This Page Blank (uspto)***



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: August 30, 2005, 11:34:25 ; Search time 46 Seconds

(without alignments)  
1898.683 Million cell updates/sec

Title: US-09-945-265-2

Perfect score: 6106  
Sequence: 1 MKQSCITVMAMALSGFFR.....DPGLKPKHKDESGGKND 1170

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summariesDatabase : Issued Patents AA: \*  
1: /cgn2\_6/ptodata/1/1aa/5A COMB pep: \*  
2: /cgn2\_6/ptodata/1/1aa/5B COMB pep: \*  
3: /cgn2\_6/ptodata/1/1aa/6A COMB pep: \*  
4: /cgn2\_6/ptodata/1/1aa/6B COMB pep: \*  
5: /cgn2\_6/ptodata/1/1aa/PTUS COMB pep: \*  
6: /cgn2\_6/ptodata/1/1aa/backfile1e1.pep: \*Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6098	99.9	1170	2	US-08-789-078-2
2	6098	99.9	1170	2	US-08-752-633-2
3	6098	99.9	1170	5	PCT-US95-04886-2
4	6058	99.2	1170	2	US-08-476-062A-42
5	6058	99.2	1170	5	PCT-US96-01314-42
6	5533.5	90.6	1065	3	US-08-630-172-9
7	5533.5	90.6	1065	3	US-09-375-419-9
8	1563	25.6	1153	1	US-08-173-497-3
9	1563	25.6	1153	1	US-08-286-889-3
10	1563	25.6	1153	1	US-08-485-618-3
11	1563	25.6	1153	1	US-08-362-652-3
12	1563	25.6	1153	2	US-08-605-672-3
13	1563	25.6	1153	2	US-08-482-293A-3
14	1563	25.6	1153	3	US-08-943-363-3
15	1563	25.6	1153	2	US-08-193-043-3
16	1563	25.6	1153	4	US-09-688-307A-3
17	1563	25.6	1153	4	US-09-350-259-3
18	1561.5	25.6	1152	4	US-08-476-062A-43
19	1561.5	25.6	1152	5	PCT-US96-01314-43
20	1561.5	25.6	1152	6	5424399-2
21	1561.5	25.6	1152	6	5424399-2
22	1521.5	24.9	1163	2	US-08-476-062A-44
23	1521.5	24.9	1163	5	PCT-US96-01314-44
24	1504	24.6	1161	3	US-09-193-043-55
25	1504	24.6	1161	4	US-09-688-307A-55
26	1504	24.6	1161	4	US-09-350-259-55
27	1496	24.5	1161	1	US-08-485-618-55

28	1496	24.5	1161	1	US-08-362-652-55	Sequence 55, Appl
29	1496	24.5	1161	2	US-08-605-672-55	Sequence 55, Appl
30	1496	24.5	1161	2	US-08-482-293A-55	Sequence 55, Appl
31	1496	24.5	1161	2	US-08-943-363-55	Sequence 55, Appl
32	1490	24.4	1161	1	US-08-485-618-53	Sequence 53, Appl
33	1490	24.4	1161	1	US-08-362-652-53	Sequence 53, Appl
34	1490	24.4	1161	2	US-08-605-672-53	Sequence 53, Appl
35	1490	24.4	1161	2	US-08-482-293A-53	Sequence 53, Appl
36	1490	24.4	1161	2	US-08-943-363-53	Sequence 53, Appl
37	1490	24.4	1161	3	US-09-193-043-53	Sequence 53, Appl
38	1490	24.4	1161	4	US-09-688-307A-53	Sequence 53, Appl
39	1490	24.4	1161	4	US-09-350-259-53	Sequence 53, Appl
40	1480.5	24.2	1163	1	US-08-173-497-4	Sequence 4, Appl
41	1480.5	24.2	1163	1	US-08-286-889-4	Sequence 4, Appl
42	1480.5	24.2	1163	1	US-08-485-618-4	Sequence 4, Appl
43	1480.5	24.2	1163	1	US-08-362-652-4	Sequence 4, Appl
44	1480.5	24.2	1163	2	US-08-605-672-4	Sequence 4, Appl
45	1480.5	24.2	1163	2	US-08-482-293A-4	Sequence 4, Appl

## ALIGNMENTS

RESULT 1  
US-08-789-078-2  
Sequence 2, Application US/08789078  
Patent No. 584385  
GENERAL INFORMATION:  
APPLICANT: Benedict, Stephen H.  
APPLICANT: Siahaan, Teruna  
APPLICANT: Chan, Marcia  
APPLICANT: Tibbetts, Scott  
TITLE OF INVENTION: ICAM-1/LFA-1 PEPTIDES FOR INDUCING  
TITLE OF INVENTION: IMMUNE TOLERANCE  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HOVER, WILLIAMS, TIMMONS & COLLINS  
STREET: 1101 Walnut St.  
CITY: Kansas City  
STATE: MO  
COUNTRY: USA  
ZIP: 64106  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/789, 078  
FILING DATE: 03-FEB-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/229, 513  
FILING DATE: 19-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Collins, John M.  
REGISTRATION NUMBER: 26262  
REFERENCE/DOCKET NUMBER: 22833  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (816)474-9050  
TELEFAX: 816/474-9057  
TELEX: 434-363  
INFORMATION FOR SBO ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1170 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
CELL TYPE: T-cell  
CELL LINE: HL-60

FEATURE:  
NAME/KEY: Region  
LOCATION: 1..25  
OTHER INFORMATION: /label= signal  
OTHER INFORMATION: /note= "Signal sequence"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 32..79  
OTHER INFORMATION: /label= Repeat  
OTHER INFORMATION: /note= "Repeat I"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 82..132  
OTHER INFORMATION: /label= Repeat  
OTHER INFORMATION: /note= "Repeat II"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 339..391  
OTHER INFORMATION: /label= Repeat  
OTHER INFORMATION: /note= "Repeat III"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 392..446  
OTHER INFORMATION: /label= Repeat  
OTHER INFORMATION: /note= "Repeat IV"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 447..508  
OTHER INFORMATION: /label= Repeat  
OTHER INFORMATION: /note= "Repeat V"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 509..567  
OTHER INFORMATION: /label= Repeat  
OTHER INFORMATION: /note= "Repeat VI"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 568..629  
OTHER INFORMATION: /label= Repeat  
OTHER INFORMATION: /note= "Repeat VII"  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 170..349  
OTHER INFORMATION: /label= IDomain  
OTHER INFORMATION: /note= "I-Domain"  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 1089..1112  
OTHER INFORMATION: /label= Trans  
OTHER INFORMATION: /note= "Transmembrane Domain"  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 1113..1170  
OTHER INFORMATION: /label= Cyto  
OTHER INFORMATION: /note= "Cytoplasmic domain"  
PUBLICATION INFORMATION:  
AUTHORS: Pigott,  
TITLE: LFA-1 Amino acid sequence (alpha) (from  
JOURNAL: PMA-stimulated HL-60 cells)  
PAGES: 94-95  
DATE: 1993  
RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1 TO 1170  
US-08-789-078-2  
Query Match 99.9%; Score 6098; DB 2; Length 1170;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MKDSCITVAMAMALISGFFPAPASSYNLDVRGARSFSPPRAGRHFGRVLTQVNGVTVGA 60  
DB 1 MKDSCITVAMAMALISGFFPAPASSYNLDVRGARSFSPPRAGRHFGRVLTQVNGVTVGA 60

QY 61 PGEKNGSTGSLYOCQSGTGCHLPVTLRGSNYTSKYLGMTLATDPTDSSIIACDPGLSRTCD 120  
DB 61 PGEKNGSTGSLYOCQSGTGCHLPVTLRGSNYTSKYLGMTLATDPTDSSIIACDPGLSRTCD 120  
QY 121 QNTYISGLCYLFRONTQGPMLQGRPGPQECIKGNVDLVPLFDGSMGLQDPDFOKIIDPMK 180  
DB 121 QNTYISGLCYLFRONTQGPMLQGRPGPQECIKGNVDLVPLFDGSMGLQDPDFOKIIDPMK 180  
QY 181 DVNKKLSNTSYCPAAVQFSTSYTEFDFSDYVWKPDALRKVKMLLTNTFGALINVY 240  
DB 181 DVNKKLSNTSYCPAAVQFSTSYTEFDFSDYVWKPDALRKVKMLLTNTFGALINVY 240  
QY 241 ATVFEEBELGARDPATKVLIIITDGEATDSGNIDAKDIIIRYIIGIKHFORKESEOTLLH 300  
DB 241 ATVFEEBELGARDPATKVLIIITDGEATDSGNIDAKDIIIRYIIGIKHFORKESEOTLLH 300  
QY 301 KFAKSPASEFVKILDTPEKIKDLFTELQKKIYIEGTSKODLTSFMNELSSSGISADLSR 360  
DB 301 KFAKSPASEFVKILDTPEKIKDLFTELQKKIYIEGTSKODLTSFMNELSSSGISADLSR 360  
QY 361 GHAVVGAAGKADWAGFLDKADLQDDPTLGNELTPEVRAGLYGTVTMLPSROKTSLL 420  
DB 361 GHAVVGAAGKADWAGFLDKADLQDDPTLGNELTPEVRAGLYGTVTMLPSROKTSLL 420  
QY 421 ASGAPRYOHMGRVTLFQEPQGGHMSQVOTIHGTQIGSYFGGELCGVDVDQDETLLLI 480  
DB 421 ASGAPRYOHMGRVTLFQEPQGGHMSQVOTIHGTQIGSYFGGELCGVDVDQDETLLLI 480  
QY 481 GADLPYGEORGKRVFIYQRRLQGFEEVSELQDQPGYPLGRFGAITALTDINDGGLVDVA 540  
DB 481 GADLPYGEORGKRVFIYQRRLQGFEEVSELQDQPGYPLGRFGAITALTDINDGGLVDVA 540  
QY 541 VGAPLEBQGANVYFNBRHGLSPQSORIEGTVLSGIGQWFGSHGVNDLBSGLADVA 600  
DB 541 VGAPLEBQGANVYFNBRHGLSPQSORIEGTVLSGIGQWFGSHGVNDLBSGLADVA 600  
QY 601 VGEASQMIYLSRPVVDMTLMSFSPAELPVHEVECSYSTSNMKEGVNTTICFOIKSLY 660  
DB 601 VGEASQMIYLSRPVVDMTLMSFSPAELPVHEVECSYSTSNMKEGVNTTICFOIKSLY 660  
QY 661 POFQGRLVANLYTTLQDGHRTTRRGLPGRGHELRNLTAVTTSMSCTDPSFHPVYVOD 720  
DB 661 POFQGRLVANLYTTLQDGHRTTRRGLPGRGHELRNLTAVTTSMSCTDPSFHPVYVOD 720  
QY 721 LISPIVUSINFSIMBEGTPRDQAGKDIPLLRPSLHSETEIPPEKXCGDKCEAN 780  
DB 721 LISPIVUSINFSIMBEGTPRDQAGKDIPLLRPSLHSETEIPPEKXCGDKCEAN 780  
QY 781 LRVSFSPARSRALRLTAFASLSYELSLSNLEBDAYWQDLHPPGLSFAKVMELKPHSQ 840  
DB 781 LRVSFSPARSRALRLTAFASLSYELSLSNLEBDAYWQDLHPPGLSFAKVMELKPHSQ 840  
QY 841 IPVSCBELPESRSLSRALSCNVSSPIPKAGSHVALQMMENTLVNSWGDVELHANVC 900  
DB 841 IPVSCBELPESRSLSRALSCNVSSPIPKAGSHVALQMMENTLVNSWGDVELHANVC 900  
QY 901 NMEDSDLEBNSATTTIIPILYPINILIQOEDSTLYVSFTPKPKKHQVKNMQUVLIOPS 960  
DB 901 NMEDSDLEBNSATTTIIPILYPINILIQOEDSTLYVSFTPKPKKHQVKNMQUVLIOPS 960  
QY 961 IHDHNIPTLEAVVGVPOPSESGPITHQMSVQMPVPYCHYEDLERLPDAEPCLPGLAFR 1020  
DB 961 IHDHNIPTLEAVVGVPOPSESGPITHQMSVQMPVPYCHYEDLERLPDAEPCLPGLAFR 1020  
QY 1021 CPVVFQGEILIVQYIGTLELVGRIEASSMFLCSLSISFNSXGPHLYGSNASTLAQVMK 1080  
DB 1021 CPVVFQGEILIVQYIGTLELVGRIEASSMFLCSLSISFNSXGPHLYGSNASTLAQVMK 1080  
QY 1081 VDVVYERKQMLYLYVLSIGILLILLIIFLYLVYVGFPRKRLKRMKRAGRVNPNGIPAE 1140  
DB 1081 VDVVYERKQMLYLYVLSIGILLILLIIFLYLVYVGFPRKRLKRMKRAGRVNPNGIPAE 1140

Qy 1141 EQLASGEAGDPGLKPLHEKDSSEGGKD 1170  
Db 1141 EQLASGEAGDPGLKPLHEKDSSEGGKD 1170

RESULT 2  
US-08-752-633-2  
; Sequence 2, Application US/08752633  
; Patent No. 5863889

GENERAL INFORMATION:  
APPLICANT: Benedict, Stephen H.  
APPLICANT: Sahaan, Teruna  
APPLICANT: Chan, Marcia  
APPLICANT: Tibbetts, Scott  
TITLE OF INVENTION: ICAM-1/LFA-1 PEPTIDES FOR INDUCING  
NUMBER OF INVENTION: IMMUNE TOLERANCE  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS  
STREET: 1101 Walnut St.  
CITY: Kansas City  
STATE: MO  
COUNTRY: USA  
ZIP: 64106

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/752,633  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Collins, John M.  
REGISTRATION NUMBER: 26262  
REFERENCE/DOCKET NUMBER: 22833  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (816)474-9050  
TELEFAX: (816)474-9057  
TELEX: 434-363

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1170 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
CELL TYPE: T-cell  
CELL LINE: HL-60

FEATURE:  
NAME/KEY: Region  
LOCATION: 1..25  
OTHER INFORMATION: /label= signal  
OTHER INFORMATION: /note= "Signal sequence"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 32..79  
OTHER INFORMATION: /label= Repeat  
OTHER INFORMATION: /note= "Repeat I"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 82..132  
OTHER INFORMATION: /label= Repeat  
OTHER INFORMATION: /note= "Repeat II"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 339..391  
OTHER INFORMATION: /label= Repeat  
OTHER INFORMATION: /note= "Repeat III"

NAME/KEY: Region  
LOCATION: 392..446  
OTHER INFORMATION: /label= Repeat  
OTHER INFORMATION: /note= "Repeat IV"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 447..508  
OTHER INFORMATION: /label= Repeat  
OTHER INFORMATION: /note= "Repeat V"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 509..567  
OTHER INFORMATION: /label= Repeat  
OTHER INFORMATION: /note= "Repeat VI"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 568..629  
OTHER INFORMATION: /label= Repeat  
OTHER INFORMATION: /note= "Repeat VII"  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 170..349  
OTHER INFORMATION: /label= IDomain  
OTHER INFORMATION: /note= "I-Domain"  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 1089..1112  
OTHER INFORMATION: /label= Trans  
OTHER INFORMATION: /note= "Transmembrane Domain"  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 1113..1170  
OTHER INFORMATION: /label= Cyto  
OTHER INFORMATION: /note= "Cytoplasmic domain"  
PUBLICATION INFORMATION:  
AUTHORS: Pigott,  
TITLE: LFA-1 Amino acid sequence (alpha) (from  
JOURNAL: PMA-stimulated HL-60 cells)  
PAGES: 94-95  
DATE: 1993  
RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1 TO 1170  
US-08-752-633-2

Query Match 99.9%; Score 6098; DB 2; Length 1170;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKDSCITVWAMALLSGFFFPAPASSYNDVKGARSSPPRAGHFGYRLQVNGYIVGA 60  
Db 1 MKDSCITVWAMALLSGFFFPAPASSYNDVKGARSSPPRAGHFGYRLQVNGYIVGA 60

Qy 61 PGRGNSGSLYQOQSGTGCLPTVLRGNSYTSKYLGMTLATDPTDGSILA CDGLSRTCD 120  
Db 61 PGRGNSGSLYQOQSGTGCLPTVLRGNSYTSKYLGMTLATDPTDGSILA CDGLSRTCD 120

Qy 121 QNTYLSGLCYLFRONTQGPMLQGRPGFORCIGKGNVDLVEFLDGSMSLQDPFOKIIDFMK 180  
Db 121 QNTYLSGLCYLFRONTQGPMLQGRPGFORCIGKGNVDLVEFLDGSMSLQDPFOKIIDFMK 180

Qy 181 DVNKKLSNTSYQPAVQFSTSYTEBFDSDYVRKQDPDALLKRVKMLLTNTFGAIIYV 240  
Db 181 DVNKKLSNTSYQPAVQFSTSYTEBFDSDYVRKQDPDALLKRVKMLLTNTFGAIIYV 240

Qy 241 ATEVFPREELGARDPAKVLIIITDGEATDSGNIDAKDIIIRYIIIGKHQTESQETIH 300  
Db 241 ATEVFPREELGARDPAKVLIIITDGEATDSGNIDAKDIIIRYIIIGKHQTESQETIH 300

Qy 301 KPASKPASEFVKILDTFEKIKDLFTLEOKKIYVIGSTSKODLTSFNMELSSSGISADLSR 360  
Db 301 KPASKPASEFVKILDTFEKIKDLFTLEOKKIYVIGSTSKODLTSFNMELSSSGISADLSR 360

QY 361 GAAVAGVAGKADWAGFLDKADLQDDTFIGNEPLEVEVAGYLGYYTWLPSRQKTSLL 420  
DB 361 GAAVAGVAGKADWAGFLDKADLQDDTFIGNEPLEVEVAGYLGYYTWLPSRQKTSLL 420  
QY 421 ASAPRYOHNGRRLLEQEPQGGHMSVOVTHGTQGSYRGGLCGVDVNDDETELLI 480  
DB 421 ASAPRYOHNGRRLLEQEPQGGHMSVOVTHGTQGSYRGGLCGVDVNDDETELLI 480  
QY 481 GABLFYGEORGRVFIYORRQLGFEVESELOQDPCGYLGRFGBAITATDINDGLADVA 540  
DB 481 GABLFYGEORGRVFIYORRQLGFEVESELOQDPCGYLGRFGBAITATDINDGLADVA 540  
QY 541 VGAPLEBQAGVYIFNGRHGGLSPQSPRIEQTQVLSGIQMGFSGIHGVKLEBDGLADVA 600  
DB 541 VGAPLEBQAGVYIFNGRHGGLSPQSPRIEQTQVLSGIQMGFSGIHGVKLEBDGLADVA 600  
QY 601 VGASQMTVLSRPVDMVTLMSPSPALIVHEVECSYSTSNMKBEVNITTCQKSLY 660  
DB 601 VGASQMTVLSRPVDMVTLMSPSPALIVHEVECSYSTSNMKBEVNITTCQKSLY 660  
QY 661 POFQGRLVANLYTLQDGHRTRRRGLFPGGRHRLRNIAVTTSMSCCTDFSPFPCVOD 720  
DB 661 POFQGRLVANLYTLQDGHRTRRRGLFPGGRHRLRNIAVTTSMSCCTDFSPFPCVOD 720  
QY 721 LISPINVSINFSIMEBGTPRDPAQGDIPILRPSLHSEWEIPEKXCGEDKCEAN 780  
DB 721 LISPINVSINFSIMEBGTPRDPAQGDIPILRPSLHSEWEIPEKXCGEDKCEAN 780  
QY 781 LRVSPSPARSRRLRTAFASLSVELSLNLEBDAYWQDLHPFGLSFRKVMELKPHSQ 840  
DB 781 LRVSPSPARSRRLRTAFASLSVELSLNLEBDAYWQDLHPFGLSFRKVMELKPHSQ 840  
QY 841 IPVSCBELPESRLLSRALSCLNVSSPIFKAGHSVALOMENFVNSWGDSEVELHANVTC 900  
DB 841 IPVSCBELPESRLLSRALSCLNVSSPIFKAGHSVALOMENFVNSWGDSEVELHANVTC 900  
QY 901 NNBSDDLBNDSATTTIIPILYPINILIQDQEDSTLYVSTPKPKIHQVQMTQVRIOPS 960  
DB 901 NNBSDDLBNDSATTTIIPILYPINILIQDQEDSTLYVSTPKPKIHQVQMTQVRIOPS 960  
QY 961 IHNNIPTLEAVGVQVPPSEGPITTHQWSQVMEPPVCHEDLERLPDAEPCLPGLAFR 1020  
DB 961 IHNNIPTLEAVGVQVPPSEGPITTHQWSQVMEPPVCHEDLERLPDAEPCLPGLAFR 1020  
QY 1021 CPVFRQELIVQYIGTLELVGEIEASSMFLCSSLSISFNSSKHFLYGSNABLAQVVMK 1080  
DB 1021 CPVFRQELIVQYIGTLELVGEIEASSMFLCSSLSISFNSSKHFLYGSNABLAQVVMK 1080  
QY 1081 VDVYERKOMLYIVLSGIGILLILLIFIVLVYVGFPRKMLKEKMEAGRGVPGIPEADS 1140  
DB 1081 VDVYERKOMLYIVLSGIGILLILLIFIVLVYVGFPRKMLKEKMEAGRGVPGIPEADS 1140  
QY 1141 EQLASQGEADPGCLKPLHEKDESGGK 1170  
DB 1141 EQLASQGEADPGCLKPLHEKDESGGK 1170

RESULT 3  
PCT-US95-04886-2  
Sequence 2, Application PC/TUS9504886

GENERAL INFORMATION:  
APPLICANT: Benedict, Stephen H.  
APPLICANT: Sibaah, Teruna  
APPLICANT: Chan, Marcia  
APPLICANT: Tibbets, Scott  
TITLE OF INVENTION: ICAM-1/LFA-1 PEPTIDES FOR INDUCING  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS  
STREET: 1101 Walnut St.  
CITY: Kansas City  
STATE: MO

COUNTRY: USA  
ZIP: 64106  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04886  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Collins, John M.  
REGISTRATION NUMBER: 26262  
REFERENCE/DOCKET NUMBER: 22833  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (816)474-9050  
TELEFAX: (816)474-9057  
TELEX: 434-363  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1170 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
CELL TYPE: T-cell  
CELL LINE: HL-60  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..25  
OTHER INFORMATION: /label= signal  
OTHER INFORMATION: /note= "Signal sequence"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 32..79  
OTHER INFORMATION: /label= Repeat  
OTHER INFORMATION: /note= "Repeat I"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 82..132  
OTHER INFORMATION: /label= Repeat  
OTHER INFORMATION: /note= "Repeat II"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 339..391  
OTHER INFORMATION: /label= Repeat  
OTHER INFORMATION: /note= "Repeat III"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 392..446  
OTHER INFORMATION: /label= Repeat  
OTHER INFORMATION: /note= "Repeat IV"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 447..508  
OTHER INFORMATION: /label= Repeat  
OTHER INFORMATION: /note= "Repeat V"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 509..567  
OTHER INFORMATION: /label= Repeat  
OTHER INFORMATION: /note= "Repeat VI"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 568..629  
OTHER INFORMATION: /label= Repeat  
OTHER INFORMATION: /note= "Repeat VII"  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 170..349

```

OTHER INFORMATION: /label= IDomain
OTHER INFORMATION: /note= "I-Domain"
FEATURE:
NAME/KEY: Domain
LOCATION: 1089..1112
OTHER INFORMATION: /label= Trans
OTHER INFORMATION: /note= "Transmembrane Domain"
FEATURE:
NAME/KEY: Domain
LOCATION: 1113..1170
OTHER INFORMATION: /label= Cyto
OTHER INFORMATION: /note= "Cytoplasmic domain"
PUBLICATION INFORMATION:
AUTHORS: Pigott,
TITLE: LFA-1 Amino acid sequence (alpha) (from
JOURNAL: The Adhesion Molecule Facts Book
PAGES: 94-95
DATE: 1993
RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1 TO 1170
PCT-US95-0486-2

```

```

Query Match          99.9%; Score 6098; DB 5; Length 1170;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 MKDSCTVMAMALLSGFFFPAPASSYNLDVARGASFSPPRGRHFGYRVLDVNGVTVGA 60
DB 1 MKDSCTVMAMALLSGFFFPAPASSYNLDVARGASFSPPRGRHFGYRVLDVNGVTVGA 60
QY 61 PDBENSTGSLYQCCSGTGHCLPVTLRSGNTSKLGMTLATDPDGSILACDPGLSTCTD 120
DB 61 PDBENSTGSLYQCCSGTGHCLPVTLRSGNTSKLGMTLATDPDGSILACDPGLSTCTD 120
QY 121 QNTYLSGLCYLFRONLQGPMLQGRPGROECIKGNVDLVPLDGSMSLQDPDFOKILDFMK 180
DB 121 QNTYLSGLCYLFRONLQGPMLQGRPGROECIKGNVDLVPLDGSMSLQDPDFOKILDFMK 180
QY 181 DVMKSLNTSYQFAAVOSTSYKTEPFDSDYVKRKPDAKLVKHMILLNTFGALNVY 240
DB 181 DVMKSLNTSYQFAAVOSTSYKTEPFDSDYVKRKPDAKLVKHMILLNTFGALNVY 240
QY 241 ATEVFRRELGRPATVLIITDGEATDSNDIAADIIIRYIIGIKGHQTKESQETLH 300
DB 241 ATEVFRRELGRPATVLIITDGEATDSNDIAADIIIRYIIGIKGHQTKESQETLH 300
QY 301 KFAKSPASBEFKILDTPEKLDLFTLEOKKIYVEGSKODLTSFNNELSSSGISADLSR 360
DB 301 KFAKSPASBEFKILDTPEKLDLFTLEOKKIYVEGSKODLTSFNNELSSSGISADLSR 360
QY 361 GHAVVAGVAGAKDWAAGFLDKADLQDDTFIGNEBLTPEVARGYLGTVTMLPSRQKTSLL 420
DB 361 GHAVVAGVAGAKDWAAGFLDKADLQDDTFIGNEBLTPEVARGYLGTVTMLPSRQKTSLL 420
QY 421 ASGAPRYQHMGRVILLFOEPQGGHMSQVQTIHGTOISYFGGELCGVDVQDGETELLII 480
DB 421 ASGAPRYQHMGRVILLFOEPQGGHMSQVQTIHGTOISYFGGELCGVDVQDGETELLII 480
QY 481 GAPLFGEOGRGRFITYOROLGFEERYSELQGDGPGYLGRRGELITLTLINDGLADVA 540
DB 481 GAPLFGEOGRGRFITYOROLGFEERYSELQGDGPGYLGRRGELITLTLINDGLADVA 540
QY 541 VGAPLEBOGAVYLFNGRHGSLPQPSQRIEGTVLSGIQWFGSRHGVKDLLEGDLADVA 600
DB 541 VGAPLEBOGAVYLFNGRHGSLPQPSQRIEGTVLSGIQWFGSRHGVKDLLEGDLADVA 600
QY 601 VQABSOQIVLSSRPVDMVTLMSPAPLIVHEVECSYSTSNKKEGVNTTICFOIKSLY 660
DB 601 VQABSOQIVLSSRPVDMVTLMSPAPLIVHEVECSYSTSNKKEGVNTTICFOIKSLY 660
QY 661 PORGRLVANLTYTLQDGHRTTRRGFLPGGRHLEARNIAVTTSMSTDSFHPVQVD 720
DB 661 PORGRLVANLTYTLQDGHRTTRRGFLPGGRHLEARNIAVTTSMSTDSFHPVQVD 720

```

```

DB 661 PORGRLVANLTYTLQDGHRTTRRGFLPGGRHLEARNIAVTTSMSTDSFHPVQVD 720
QY 721 LISPIVNSLNPGLMEBEGTTPDQPAQCKDIPLIRPSLHSETWEIPPEKNCGEDKCEAN 780
DB 721 LISPIVNSLNPGLMEBEGTTPDQPAQCKDIPLIRPSLHSETWEIPPEKNCGEDKCEAN 780
QY 781 LRVSPARSRAIRLRTAFASLVELSLSNLEDAVWQDLHPHPPGLSFPKVKELKPHSQ 840
DB 781 LRVSPARSRAIRLRTAFASLVELSLSNLEDAVWQDLHPHPPGLSFPKVKELKPHSQ 840
QY 841 IPVSCBELPRESRLSRALSQNVSPPIFKAGSHVALQMENTLVNSWGDVSELAHAYTC 900
DB 841 IPVSCBELPRESRLSRALSQNVSPPIFKAGSHVALQMENTLVNSWGDVSELAHAYTC 900
QY 901 NNEBSDLLEDNSATTTIIPILYINILIQDQEDSTLYVSTPKGPKIHQVMTQVRIOPS 960
DB 901 NNEBSDLLEDNSATTTIIPILYINILIQDQEDSTLYVSTPKGPKIHQVMTQVRIOPS 960
QY 961 IHDHNPITLAAVGVPPSPSEGPITTHQMSVQMBEPVPCHEDELERLPDAAPCLPGLAFR 1020
DB 961 IHDHNPITLAAVGVPPSPSEGPITTHQMSVQMBEPVPCHEDELERLPDAAPCLPGLAFR 1020
QY 1021 CPVVFROELIVQYIGTLELVGIEASQMFSLCSLSISFNSKHFHLVGSNASTLAQVVMK 1080
DB 1021 CPVVFROELIVQYIGTLELVGIEASQMFSLCSLSISFNSKHFHLVGSNASTLAQVVMK 1080
QY 1081 VDVIYERKQMLYLYLSGIGLLILLIIFVLYKVGFEKRLKERMAGRGVNPNGIPADS 1140
DB 1081 VDVIYERKQMLYLYLSGIGLLILLIIFVLYKVGFEKRLKERMAGRGVNPNGIPADS 1140
QY 1141 EQLASQGEADPGCLKPLHKKDSGSGKD 1170
DB 1141 EQLASQGEADPGCLKPLHKKDSGSGKD 1170

```

```

RESULT 4
US-08-476-062A-42
Sequence 42, Application US/08476062A
Patent No. 5877275
GENERAL INFORMATION:
APPLICANT: Arnaout, M. Amin
TITLE OF INVENTION: CONTROLLING CELLULAR IMMUNE/INFLAMMATORY
TITLE OF INVENTION: RESPONSES WITH BETA2 INTEGRINS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,062A
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/216,081
FILING DATE: 21-MAR-1994
APPLICATION NUMBER: 07/637,830
FILING DATE: 04-JAN-1991
APPLICATION NUMBER: 07/539,842
FILING DATE: 18-JUN-1990
APPLICATION NUMBER: 07/212,573
FILING DATE: 28-JUN-1988
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00786/068003
TELECOMMUNICATION INFORMATION:

```

TELEPHONE: 617/542-5070  
 TELEFAX: 617/542-8906  
 TELEX: 200154  
 INFORMATION FOR SEQ ID NO: 42:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1170 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 US-08-476-062A-42

Query Match 99.2%; Score 6058; DB 2; Length 1170;  
 Best Local Similarity 99.4%; Pred. No. 0;

Matches 1163; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 MKDSCITVAMALLSGFFFPAPASSYNLDVRGARSPFPRAHGFGRVLYQVNGVYVGA 60  
 DB 1 MKDSCITVAMALLSGFFFPAPASSYNLDVRGARSPFPRAHGFGRVLYQVNGVYVGA 60  
 QY 61 PGGNNTGSLYOCOSGTHCLPTLNGSNYSKYLGMTLATDPTDGSILACDPELSRTCD 120  
 DB 61 PGGNNTGSLYOCOSGTHCLPTLNGSNYSKYLGMTLATDPTDGSILACDPELSRTCD 120  
 QY 121 QNTYLSGLCYLFRONTQGPMLQGRPGFQECIKGNVDLVFLFDGSMSLQDPEFKILDPMK 180  
 DB 121 QNTYLSGLCYLFRONTQGPMLQGRPGFQECIKGNVDLVFLFDGSMSLQDPEFKILDPMK 180  
 QY 181 DVWKKLSNYSYQPAVQFSTSYTERPFSYVKRQDPAKLLKVKHMLLTNTFGALINY 240  
 DB 181 DVWKKLSNYSYQPAVQFSTSYTERPFSYVKRQDPAKLLKVKHMLLTNTFGALINY 240  
 QY 241 ATAVFREBELGARPDATVLIITDGEATDSGNIIDAKDIIIRYIIGIKHFKOTKESQETLH 300  
 DB 241 ATAVFREBELGARPDATVLIITDGEATDSGNIIDAKDIIIRYIIGIKHFKOTKESQETLH 300  
 QY 301 KFAASKPASEFVKILDTPEKLDLFTLEQKIIYVLEGSTKODLTSFNNELSSSGISADLSR 360  
 DB 301 KFAASKPASEFVKILDTPEKLDLFTLEQKIIYVLEGSTKODLTSFNNELSSSGISADLSR 360  
 QY 361 GHAVVGAAGKAWAGGFLDKADLQDPTFGNEPLTEPVAGIYGYVTWLPBROKTSLL 420  
 DB 361 GHAVVGAAGKAWAGGFLDKADLQDPTFGNEPLTEPVAGIYGYVTWLPBROKTSLL 420  
 QY 421 ASAPRYQHNGRYLLFQEPQGGGMSQVQIHTQISYFGSELGCVDVQDSETELLI 480  
 DB 421 ASAPRYQHNGRYLLFQEPQGGGMSQVQIHTQISYFGSELGCVDVQDSETELLI 480  
 QY 481 GAFLFYGEORGRVFIYORQQLGFEVSELQGDPEYPLGRFGAITALTDINGDLVDA 540  
 DB 481 GAFLFYGEORGRVFIYORQQLGFEVSELQGDPEYPLGRFGAITALTDINGDLVDA 540  
 QY 541 VGAPLEBQAVYIFNGRHGSLSPQSORIGTQVLSGIQWFGSIHVKULBEGDLADVA 600  
 DB 541 VGAPLEBQAVYIFNGRHGSLSPQSORIGTQVLSGIQWFGSIHVKULBEGDLADVA 600  
 QY 601 VGBESQWIVASRPVDMVTLMSPSPARIVHEVECSYSTSNMKKEGWNITICQIKSLY 660  
 DB 601 VGBESQWIVASRPVDMVTLMSPSPARIVHEVECSYSTSNMKKEGWNITICQIKSLY 660  
 QY 661 POFQGRLVANITYTLQDGHRTTRRGFLPGSRHLEARNIIVTSSMCTDPSFHPVQVD 720  
 DB 661 POFQGRLVANITYTLQDGHRTTRRGFLPGSRHLEARNIIVTSSMCTDPSFHPVQVD 720  
 QY 721 LIPIPVNSLNFSLMEBGTPRDQAGKDIPIIIRPSLHSEIWEIPEKNCGEKCEAN 780  
 DB 721 LIPIPVNSLNFSLMEBGTPRDQAGKDIPIIIRPSLHSEIWEIPEKNCGEKCEAN 780  
 QY 781 LRVSFSPARSARALRTFASLSVELSLSNLEBDAYWQOLDHPPGSGFKKVEKLKHSQ 840  
 DB 781 LRVSFSPARSARALRTFASLSVELSLSNLEBDAYWQOLDHPPGSGFKKVEKLKHSQ 840  
 QY 841 IPVSCBELPESRSLSRALSQNVSSPIFKAGHSVALQMMFNTLVNNSWGDVSELIHANTVC 900

DB 841 IPVSCBELPESRSLSRALSQNVSSPIFKAGHSVALQMMFNTLVNNSWGDVSELIHANTVC 900  
 QY 901 NNEDSDLEDNASTTIPILYPIINILIOQDESTLYVSPKGPKHQVKNYQVFIQS 960  
 DB 901 NNEDSDLEDNASTTIPILYPIINILIOQDESTLYVSPKGPKHQVKNYQVFIQS 960  
 QY 961 IHDHNIPTLEAVGVQPPSEBPTIHWQSVQMEPPVPCHEDELRLPDAAEPCLEPPLR 1020  
 DB 961 IHDHNIPTLEAVGVQPPSEBPTIHWQSVQMEPPVPCHEDELRLPDAAEPCLEPPLR 1020  
 QY 1021 CPVFFRQELIVQYIGLELVGEIISASWFSLCSSLSISFNSSKHFTLYGSNLSAQVNMK 1080  
 DB 1021 CPVFFRQELIVQYIGLELVGEIISASWFSLCSSLSISFNSSKHFTLYGSNLSAQVNMK 1080  
 QY 1081 VDVVYEKQMLYLYVLSIGLILLILIFVLVYKGFERNLKEKMGAGRVNGIPEADS 1140  
 DB 1081 VDVVYEKQMLYLYVLSIGLILLILIFVLVYKGFERNLKEKMGAGRVNGIPEADS 1140  
 QY 1141 EQLASQGEADPGCLKPLHEKXESGSGKD 1170  
 DB 1141 EQLASQGEADPGCLKPLHEKXESGSGKD 1170

# RESULT 5 PCT-US96-01314-42

Sequence 42, Application PC/TUS9601314

GENERAL INFORMATION:

APPLICANT: M. Amin Arnaut

TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN

TITLE OF INVENTION: ANTAGONISTS

NUMBER OF SEQUENCES: 78

CORRESPONDENCE ADDRESS:

ADDRESSER: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 MB

COMPUTER: IBM PS/2 Model 502 or 555X

OPERATING SYSTEM: MS-DOS (Version 5.0)

SOFTWARE: Wordperfect (Version 5.1)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/01314

FILING DATE: 30-JAN-96

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/380,167

FILING DATE: 30-JAN-95

ATTORNEY/AGENT INFORMATION:

NAME: John W. Freeman

REGISTRATION NUMBER: 29,066

REFERENCE/DOCKET NUMBER: 00786/267001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 42:

SEQUENCE CHARACTERISTICS:

LENGTH: 1170

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

PCT-US96-01314-42

Query Match 99.2%; Score 6058; DB 5; Length 1170;  
 Best Local Similarity 99.4%; Pred. No. 0;  
 Matches 1163; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 MKDSCITVAMALLSGFFFPAPASSYNLDVRGARSPFPRAHGFGRVLYQVNGVYVGA 60  
 DB 1 MKDSCITVAMALLSGFFFPAPASSYNLDVRGARSPFPRAHGFGRVLYQVNGVYVGA 60

QY 61 PGBENSTGSLYQCCSGTGCHCLPVTLRGNSNTSKYLGMTLATDPTDGSLLACDPGLSRCPD 120  
 DB 61 PGBENSTGSLYQCCSGTGCHCLPVTLRGNSNTSKYLGMTLATDPTDGSLLACDPGLSRCPD 120  
 QY 121 QNTYLSGLCYLFRONTQGPMLQGRPGFQECIKGNVLDVFLPDGSMSLQDPDFQKILDPMK 180  
 DB 121 QNTYLSGLCYLFRONTQGPMLQGRPGFQECIKGNVLDVFLPDGSMSLQDPDFQKILDPMK 180  
 QY 181 DVMKLSNTSYQFAAVPSTSYKTEPSPDVYKRDADALLKHYKMLLNTTGALINY 240  
 DB 181 DVMKLSNTSYQFAAVPSTSYKTEPSPDVYKRDADALLKHYKMLLNTTGALINY 240  
 QY 241 ATEVFEELGARPRATVLIITITGBATDSNDIAADIIIRYIIIGIGHPTKESQETLH 300  
 DB 241 ATEVFEELGARPRATVLIITITGBATDSNDIAADIIIRYIIIGIGHPTKESQETLH 300  
 QY 301 KFASKPASEFVKILDTPEKLDLFTBELQKIIYIEGTSKODLTSFNNELSSSGISADLSR 360  
 DB 301 KFASKPASEFVKILDTPEKLDLFTBELQKIIYIEGTSKODLTSFNNELSSSGISADLSR 360  
 QY 361 GHAVVGAAGKADWAGFLDLKADLQDDTFIGNEBLTPBVAGYGYTVVWLPSRQKTSLL 420  
 DB 361 GHAVVGAAGKADWAGFLDLKADLQDDTFIGNEBLTPBVAGYGYTVVWLPSRQKTSLL 420  
 QY 421 ASGAPRYOHNGRYLLPQEPQCGHMSQVOTIHGQISYFGSELGVVDVQDGETELLII 480  
 DB 421 ASGAPRYOHNGRYLLPQEPQCGHMSQVOTIHGQISYFGSELGVVDVQDGETELLII 480  
 QY 481 GAFPLYEGORGRVFIYQRRQLGFEVSELQDPRGYLGRFGAIIYALTITINGGLDVA 540  
 DB 481 GAFPLYEGORGRVFIYQRRQLGFEVSELQDPRGYLGRFGAIIYALTITINGGLDVA 540  
 QY 541 VGAPLEBQAGVYIFNGRHGSLSPQSPQRIEGTVLSGIQWFGSRHGVKDLBQDGLDVA 600  
 DB 541 VGAPLEBQAGVYIFNGRHGSLSPQSPQRIEGTVLSGIQWFGSRHGVKDLBQDGLDVA 600  
 QY 601 VGASQMTIVSSRPVDMTLMSPSPAEIPVHESSYSTSNMCKEAVNTTICQIKSLY 660  
 DB 601 VGASQMTIVSSRPVDMTLMSPSPAEIPVHESSYSTSNMCKEAVNTTICQIKSLY 660  
 QY 661 POFQGRLVANLTYTLQDGHRTTRRGFLPGGRHLELRNIAVTTSMSCITDPSFHPVQVD 720  
 DB 661 POFQGRLVANLTYTLQDGHRTTRRGFLPGGRHLELRNIAVTTSMSCITDPSFHPVQVD 720  
 QY 721 LISPINVSLNFSIMEEGTPRDQRAQKDIPIILPRLSHSEWELIPEKNGCEDKCEAN 780  
 DB 721 LISPINVSLNFSIMEEGTPRDQRAQKDIPIILPRLSHSEWELIPEKNGCEDKCEAN 780  
 QY 781 LRVSPFARBARLRTAFASLSVELSINLEBDAVYQDLHPPPGLSFKPKVEMLKPHSQ 840  
 DB 781 LRVSPFARBARLRTAFASLSVELSINLEBDAVYQDLHPPPGLSFKPKVEMLKPHSQ 840  
 QY 841 IPVSCBELPRESRLSALSCNVSPIFKAGHSVALOMFNLTUNSSWGSVELHANVTC 900  
 DB 841 IPVSCBELPRESRLSALSCNVSPIFKAGHSVALOMFNLTUNSSWGSVELHANVTC 900  
 QY 901 NNEBSDLJEDNSATTTIPIILYINILIQDQEDSTLYVFTPKGPKIHQVHMTQVRIOPS 960  
 DB 901 NNEBSDLJEDNSATTTIPIILYINILIQDQEDSTLYVFTPKGPKIHQVHMTQVRIOPS 960  
 QY 961 IHDHNTFTLEAVGVPOPEBGPITTHQWSVQMEBPVCHYEDLERLDAAPCLPGALFR 1020  
 DB 961 IHDHNTFTLEAVGVPOPEBGPITTHQWSVQMEBPVCHYEDLERLDAAPCLPGALFR 1020  
 QY 1021 CPVVFROEIIVOYVIGTELVGEIEASSMFSICSSLSIFNYSKXHFHLYGSNASTLAQVVMK 1080  
 DB 1021 CPVVFROEIIVOYVIGTELVGEIEASSMFSICSSLSIFNYSKXHFHLYGSNASTLAQVVMK 1080  
 QY 1081 VDVVYEROMLYLYVLSGIGILLLLLIYLYVYKGFPRKMLKEMEAGRGVPGNIPAEBS 1140  
 DB 1081 VDVVYEROMLYLYVLSGIGILLLLLIYLYVYKGFPRKMLKEMEAGRGVPGNIPAEBS 1140

QY 1141 EQLASQGEADPGCLKPLHEKDESGGKX 1170  
 DB 1141 EQLASQGEADPGCLKPLHEKDESGGKX 1170  
 RESULT 6  
 US-08-630-172-9  
 ; Sequence 9, Application US/08630172  
 ; Patent No. 606054  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Staerz, Uwe  
 ; TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T  
 ; TITLE OF INVENTION: LYMPHOCYTE VETO  
 ; NUMBER OF SEQUENCES: 41  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Sheridan Ross & McIntosh  
 ; STREET: 1700 Lincoln Street, 35th Floor  
 ; CITY: Denver  
 ; STATE: Colorado  
 ; COUNTRY: U.S.  
 ; ZIP: 80203  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Releasee #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/630,172  
 ; FILING DATE:  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Connell, Gary J.  
 ; REGISTRATION NUMBER: 32,020  
 ; REFERENCE/DOCKET NUMBER: 2879-36  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (303) 863-9700  
 ; TELEFAX: (303) 863-0223  
 ; INFORMATION FOR SEQ ID NO: 9:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1065 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-630-172-9  
 Query Match 90.6%; Score 553.5; DB 3; Length 1065;  
 Best Local Similarity 99.6%; Pred. No. 0;  
 Matches 1061; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 26 YNIDVRGANSFSPPRARHFGYRVLOVNGVIVGAPGEGNSTGSLYQCCSGTGCHCLPVTL 85  
 DB 1 YNIDVRGANSFSPPRARHFGYRVLOVNGVIVGAPGEGNSTGSLYQCCSGTGCHCLPVTL 85  
 QY 86 RGSNTSKYLGMTLATDPTDGSLLACDPGLSRCPDQNTYLSGLCYLFRONTQGPMLQGRP 145  
 DB 86 RGSNTSKYLGMTLATDPTDGSLLACDPGLSRCPDQNTYLSGLCYLFRONTQGPMLQGRP 145  
 QY 61 RGSNTSKYLGMTLATDPTDGSLLACDPGLSRCPDQNTYLSGLCYLFRONTQGPMLQGRP 120  
 DB 61 RGSNTSKYLGMTLATDPTDGSLLACDPGLSRCPDQNTYLSGLCYLFRONTQGPMLQGRP 120  
 QY 146 GFQECIKGNVLDVFLPDGSMSLQDPDFQKILDPMKDVMKLSNTSYQFAAVPSTSYKTE 205  
 DB 146 GFQECIKGNVLDVFLPDGSMSLQDPDFQKILDPMKDVMKLSNTSYQFAAVPSTSYKTE 205  
 QY 121 GFQECIKGNVLDVFLPDGSMSLQDPDFQKILDPMKDVMKLSNTSYQFAAVPSTSYKTE 180  
 DB 121 GFQECIKGNVLDVFLPDGSMSLQDPDFQKILDPMKDVMKLSNTSYQFAAVPSTSYKTE 180  
 QY 206 FDFSDYKRDADPALLKHYKMLLNTTGALINYVADEVFEELGARPRATVLIITITDG 265  
 DB 206 FDFSDYKRDADPALLKHYKMLLNTTGALINYVADEVFEELGARPRATVLIITITDG 265  
 QY 266 EATDSNDIAADIIIRYIIIGIGHPTKESQETLHFKPASEFVKILDTPEKLDLFT 325  
 DB 266 EATDSNDIAADIIIRYIIIGIGHPTKESQETLHFKPASEFVKILDTPEKLDLFT 325  
 QY 241 EATDSNDIAADIIIRYIIIGIGHPTKESQETLHFKPASEFVKILDTPEKLDLFT 300  
 DB 241 EATDSNDIAADIIIRYIIIGIGHPTKESQETLHFKPASEFVKILDTPEKLDLFT 300  
 QY 326 ELQKKIYVIEGTSKODLTSFNNELSSSGISADLSRGHAAVGAAGKADWAGFLDLKADLQ 385  
 DB 326 ELQKKIYVIEGTSKODLTSFNNELSSSGISADLSRGHAAVGAAGKADWAGFLDLKADLQ 385  
 QY 301 ELQKKIYVIEGTSKODLTSFNNELSSSGISADLSRGHAAVGAAGKADWAGFLDLKADLQ 360  
 DB 301 ELQKKIYVIEGTSKODLTSFNNELSSSGISADLSRGHAAVGAAGKADWAGFLDLKADLQ 360



```

QY 386 DDTFIGNEPLEPRAGYLGVTWTLPSRQKTSILASGAPRYOHMGRVLLFOEPGGGHW 445
|
|
|
Db 361 DDTFIGNEPLEPRAGYLGVTWTLPSRQKTSILASGAPRYOHMGRVLLFOEPGGGHW 420
|
|
|
QY 446 SQVQTHGTQIGSYFGGELCGVDVDDGETE-LILIGAPLYGBOGRGVFIYQRQLGF 504
|
|
|
Db 421 SQVQTHGTQIGSYFGGELCGVDVDDGETE-LILIGAPLYGBOGRGVFIYQRQLGF 480
|
|
|
QY 505 EEVSEIQQDGYPLGRGGEALITLTDINGDLVDVAVGAPLEBQAVYIFNGRHGGLSPQ 564
|
|
|
Db 481 EEVSEIQQDGYPLGRGGEALITLTDINGDLVDVAVGAPLEBQAVYIFNGRHGGLSPQ 540
|
|
|
QY 565 PSORIBGTQVLSGIQWFGRSIHGKDLBGLADVAVGASQMTVLSRPVDMVTLSMF 624
|
|
|
Db 541 PSORIBGTQVLSGIQWFGRSIHGKDLBGLADVAVGASQMTVLSRPVDMVTLSMF 600
|
|
|
QY 625 SPAEIPVHEVCYSTSNKKEGVNITICFOIKSLYPOFQGRVAVNTYTLQDGHRTTR 684
|
|
|
Db 601 SPAEIPVHEVCYSTSNKKEGVNITICFOIKSLYPOFQGRVAVNTYTLQDGHRTTR 660
|
|
|
QY 685 RGLFPGGRHLRRIAVTTSMSCTDPSFHPVVCVODLISPINVSINLSMBEETPRDOR 744
|
|
|
Db 661 RGLFPGGRHLRRIAVTTSMSCTDPSFHPVVCVODLISPINVSINLSMBEETPRDOR 720
|
|
|
QY 745 AOGKDIPILRPSLHSETWEIPEKNCGBDKCEANLRVFSFSPARSALRLTAASLSVE 804
|
|
|
Db 721 AOGKDIPILRPSLHSETWEIPEKNCGBDKCEANLRVFSFSPARSALRLTAASLSVE 780
|
|
|
QY 805 LLSINLEEDAYWQDLHPPPGSLFRKVEMLKPHSQIPVSCBEPBESRLSRLSCNVS 864
|
|
|
Db 781 LLSINLEEDAYWQDLHPPPGSLFRKVEMLKPHSQIPVSCBEPBESRLSRLSCNVS 840
|
|
|
QY 865 SPIFKASHVALQMNFTLVNSWGSDVEIHAANTCNNEEDSDILEDSATITIPILYPIN 924
|
|
|
Db 841 SPIFKASHVALQMNFTLVNSWGSDVEIHAANTCNNEEDSDILEDSATITIPILYPIN 900
|
|
|
QY 925 ILIODOEDSTLYSFTFKGPKIHQVKMYQVRIOPIHIDHNIPTLEAVGVPOPPSEGP 984
|
|
|
Db 901 ILIODOEDSTLYSFTFKGPKIHQVKMYQVRIOPIHIDHNIPTLEAVGVPOPPSEGP 960
|
|
|
QY 985 THQMSVMEBPVPCHEYDLERLPDAEPCLPGALFRCPVVRROBILVQVIGTLEVEIE 1044
|
|
|
Db 961 THQMSVMEBPVPCHEYDLERLPDAEPCLPGALFRCPVVRROBILVQVIGTLEVEIE 1020
|
|
|
QY 1045 ASSMFSICSSLSISFNSSKQFHLVGSNASTLAQVVMKVVDVYEKKM 1089
|
|
|
Db 1021 ASSMFSICSSLSISFNSSKQFHLVGSNASTLAQVVMKVVDVYEKKM 1065
|
|
|

```

```

RESULT 7
US-09-375-419-9
; Sequence 9, Application US/09375419
; Patent No. 6264950
; GENERAL INFORMATION:
; APPLICANT: Staerz, Uwe
; TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, 35th Floor
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/375,419
; FILING DATE:
;

```

```

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/630,172
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2879-36
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1065 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-375-419-9
Query Match 90.6%; Score 5533.5; DB 3; Length 1065;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1061; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 26 YNLDVGAASFSPPRAGRHGYRVLYQVANGVTVGABGNGSTSLYQCOSGTGHCUPVTL 85
|
|
|
Db 1 YNLDVGAASFSPPRAGRHGYRVLYQVANGVTVGABGNGSTSLYQCOSGTGHCUPVTL 60
|
|
|
QY 86 RGSNTSKYLQMTLADPTDGSILACDPLSRICDONTYLSGLCYLFRONTLQPMLOGRP 145
|
|
|
Db 61 RGSNTSKYLQMTLADPTDGSILACDPLSRICDONTYLSGLCYLFRONTLQPMLOGRP 120
|
|
|
QY 146 GFQECIKGNVDVLELPDGSMSLOPDEFQKILDPMDKVMKLSVTSYQPAVOPSTSYKTE 205
|
|
|
Db 121 GFQECIKGNVDVLELPDGSMSLOPDEFQKILDPMDKVMKLSVTSYQPAVOPSTSYKTE 180
|
|
|
QY 206 FDFSDYVKRDPDALLKHYKMLLTNTFGAINVYAVEVREBELGARPDATKYLIIITDG 265
|
|
|
Db 181 FDFSDYVKRDPDALLKHYKMLLTNTFGAINVYAVEVREBELGARPDATKYLIIITDG 240
|
|
|
QY 266 EATDSGNIDAANDIYIIIGIKGHPOTKESQETLHFAKSPASEFYKIIDTFEKLKDLFT 325
|
|
|
Db 241 EATDSGNIDAANDIYIIIGIKGHPOTKESQETLHFAKSPASEFYKIIDTFEKLKDLFT 300
|
|
|
QY 326 ELQKTIYVIEGTSKQDLTSPNMLSSSGISADLSRGHAVVGAADWAGGFIDLKADLC 385
|
|
|
Db 301 ELQKTIYVIEGTSKQDLTSPNMLSSSGISADLSRGHAVVGAADWAGGFIDLKADLC 360
|
|
|
QY 386 DDTFIGNEPLEPRAGYLGVTWTLPSRQKTSILASGAPRYOHMGRVLLFOEPGGGHW 445
|
|
|
Db 361 DDTFIGNEPLEPRAGYLGVTWTLPSRQKTSILASGAPRYOHMGRVLLFOEPGGGHW 420
|
|
|
QY 446 SQVQTHGTQIGSYFGGELCGVDVDDGETE-LILIGAPLYGBOGRGVFIYQRQLGF 504
|
|
|
Db 421 SQVQTHGTQIGSYFGGELCGVDVDDGETE-LILIGAPLYGBOGRGVFIYQRQLGF 480
|
|
|
QY 505 EEVSEIQQDGYPLGRGGEALITLTDINGDLVDVAVGAPLEBQAVYIFNGRHGGLSPQ 564
|
|
|
Db 481 EEVSEIQQDGYPLGRGGEALITLTDINGDLVDVAVGAPLEBQAVYIFNGRHGGLSPQ 540
|
|
|
QY 565 PSORIBGTQVLSGIQWFGRSIHGKDLBGLADVAVGASQMTVLSRPVDMVTLSMF 624
|
|
|
Db 541 PSORIBGTQVLSGIQWFGRSIHGKDLBGLADVAVGASQMTVLSRPVDMVTLSMF 600
|
|
|
QY 625 SPAEIPVHEVCYSTSNKKEGVNITICFOIKSLYPOFQGRVAVNTYTLQDGHRTTR 684
|
|
|
Db 601 SPAEIPVHEVCYSTSNKKEGVNITICFOIKSLYPOFQGRVAVNTYTLQDGHRTTR 660
|
|
|
QY 685 RGLFPGGRHLRRIAVTTSMSCTDPSFHPVVCVODLISPINVSINLSMBEETPRDOR 744
|
|
|
Db 661 RGLFPGGRHLRRIAVTTSMSCTDPSFHPVVCVODLISPINVSINLSMBEETPRDOR 720
|
|
|
QY 745 AOGKDIPILRPSLHSETWEIPEKNCGBDKCEANLRVFSFSPARSALRLTAASLSVE 804
|
|
|

```

Db 721 AOGKDIPILRPSLHSETWEIPFEKNGCEBKCEANLRVSPSPARSALRLTAFASLSVE 780  
 Qy 805 LLSLNEEDAYWVOLDLHPFGSLFRKVEMLKPHSOIPVSCBELPESSRLISRLSCNVS 864  
 Db 781 LLSLNEEDAYWVOLDLHPFGSLFRKVEMLKPHSOIPVSCBELPESSRLISRLSCNVS 840  
 Qy 865 SPIKAGSHVALQWFMFTLVNSWGDVVELHANTVCNNEDSDLLJEDNSATTIIPILPIN 924  
 Db 841 SPIKAGSHVALQWFMFTLVNSWGDVVELHANTVCNNEDSDLLJEDNSATTIIPILPIN 900  
 Qy 925 ILIQDQDSTLYVSPTRPKPKIHOVKMYQVRIOPSIDHNIPTLBAVVGVPQPPSEGP 984  
 Db 901 ILIQDQDSTLYVSPTRPKPKIHOVKMYQVRIOPSIDHNIPTLBAVVGVPQPPSEGP 960  
 Qy 985 THQMSVQMPVPVPHYEDLELPAAPBCPLFGALFRCPVVPFRQILYQVIGTLELVEIE 1044  
 Db 961 THQMSVQMPVPVPHYEDLELPAAPBCPLFGALFRCPVVPFRQILYQVIGTLELVEIE 1020  
 Qy 1045 ASSWFLCSSLSISFNSSKPHFLYGSNLSLAQVVMKVQVVEKQ 1089  
 Db 1021 ASSWFLCSSLSISFNSSKPHFLYGSNLSLAQVVMKVQVVEKQ 1065

## RESULT 8

US-08-173-497-3  
 ; Sequence 3, Application US/08173497  
 ; Patent No. 5437958  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gallatin, W. Michael  
 ; APPLICANT: Van Der Vaeren, Monica  
 ; TITLE OF INVENTION: No. 5437958e1 Human 2 Integrin Alpha  
 ; NUMBER OF SEQUENCES: 29  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun  
 ; STREET: 233 S. Wacker Drive, 6300 Sears Tower  
 ; City: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: USA  
 ; ZIP: 60606-6402  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; OPERATING SYSTEM: IBM PC compatible  
 ; SOFTWARE: Patent in Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/173,497  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: No. 5437958and, Greta E.  
 ; REGISTRATION NUMBER: 35,302  
 ; REFERENCE/DOCKET NUMBER: 27866/31363  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 312-474-6300  
 ; TELEFAX: 312-474-0448  
 ; TELEX: 25-3856  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1153 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-173-497-3

Query Match 25.6%; Score 1563; DB 1; Length 1153;  
 Best Local Similarity 34.3%; Pred. No. 1.9e-124;  
 Matches 410; Conservative 210; Mismatches 464; Indels 110; Gaps 38;  
 Qy 6 ITWAMALLSGFFPAPASSYNDLVGRGSPSPRAGRSHGYRVLQY-GNGVIVGAGE- 63  
 Db 6 LILTALTLGCGF-----NLDTENAMTFQ--ENARGFGQSVVOLQSGRVVVGAFQEI 54

Qy 64 --GNSGTSLYQCCSGTGHCLPVTLR--GSNTYSKYLGTTLATDPDGSIIACDPGLSTCD 120  
 Db 55 VAAHQSGSLYQCCYVSTGSCCEPIRLQVPEAVNMSLGLSLAATTSPPQLACGPIVHTGCS 114  
 Qy 121 QNTYLSGLCYLFPQNLQGPMLQGRPGFQECIKG---NVDLVFLFDSSMSLQDPDEFQKIL 176  
 Db 115 ENTVYKLCFLFGSNLR---QDPQKPEALRCPQEDSIALILDSGSIIRHDFRMRK 170  
 Qy 177 DPMKDVKKLSNTSYQPAVQFSTYKTEPFDSDYVRKQPDALIKRVKMLLTNTFGA 236  
 Db 171 EFVSTWBLQKSKTILFSLMYSEEFRIHFTFKFQNNPMPRLSVKRIITQLGRTHTATG 230  
 Qy 237 INVATVPRBEIAGAPDARKLIIITDGR--ATDSNDIAAD----IIRYIIGKX 289  
 Db 231 IRRVRELFNITNGARNNAKILVITDGBKFDPLDEYEVIPBADREGIIRYVIGVDA 290  
 Qy 290 FQTKESQETLHKASKPASEFVKILDTPEKLDLFTLEOKIYIEGTSKODLTSFMNEL 349  
 Db 291 FRESKSRQELNTASKPRPDHVQVNNFELKTIQNLREKIRAIESTQTCSSSFHEM 350  
 Qy 350 SSSGISADLSRGHAVVAGAKDMAGGFLDKADLDDTFIGNEPIITPEVRAQYLYT 409  
 Db 351 SQSGFSAITSNGLPLSTVGSYDMAGVF-LYTSKEKSTINMTRVDSNNDAVLYGAAA 409  
 Qy 410 WLPDRQKTSILASGAPRYQMGKRVLLFQEPQGGHMSQVOTHTGTQIGTFGELCVDV 469  
 Db 410 -ILIRNVOSLVVIGAPRYQHIGLVAMFR--QNTGMESNANVGTQIGAFYGASLCVDV 466  
 Qy 470 DQGETELLIGAPLFPGEGRGRVFIY-----ORQLGFEVSELOGDGYLGRGEA 524  
 Db 467 DSNGSTDLVILGAPHYEQRGQVSCVPLPRQQRARWQCDAY--LYGEGQGPWGRGAA 524  
 Qy 525 ITALTIDNGDLVAVAGAPLEB--OGAVYIFNGRAG-GLSPQSPQRIESTQVLSGIQWF 581  
 Db 525 LTVLGVNKGKLDVVALGAGEEDNRGAVYLFHTGSGSGISPSHSQRIASKXLSPLQYF 584  
 Qy 582 GRSIHGVKDLGDLADVAVAGSOMIVLSRPVDMVTLMSPSPAIPIVHEVCYSTS 641  
 Db 585 QGSLGGQDLTMGLVDLTVGAQGHVLLRSQVLRAKALMEPNPREVANVEPCNDQV 644  
 Qy 642 NKKEGNITICQI--KSLYRQF--QGRIVANLTYTQLDCHRRRRLFGGHELRNI 699  
 Db 645 -KKEKEGEVAVCLHVKSTDRLEBQISVVTYDALSGRHSRAVEFETKNSTRQT 703  
 Qy 700 AYT--TSMSCDTDFSFHPVQVDLISPINVSINSLWEEEGTPPDQRAQKDIPILRPSL 758  
 Db 704 QVGLQYTCETLKLQPLNCIEDVPSPILVRLNFSL---VQTPLS--AFGN-----LRPV 753  
 Qy 759 HSETWEI-----PFRKNGCEBKCEANLRVSPSPARSALRLTAFASLSVELSLNEED 813  
 Db 754 ABDAQRLFTALPFEKNGCNDNICODDLSTTFMSLDCLVGGPREFNTVTVRNDGED 813  
 Qy 814 AYVAVOLDLHPPLSLRKYEML---KPHSOIPVSCBELPESSRLISRL---SCNVSPI 867  
 Db 814 SYRTVTFPPDLDSYRKVSTLONORSORSWRLACES--ASTYVGCALKSTCSINHPI 871  
 Qy 868 FKAGSHVALQWFMFTLVNSWGDVVELHANTVCNNEDSDLLJEDNSATTI---PIIYPIN 924  
 Db 872 FPNSEVTFNITVDVSKASLGNKLLKANVTSENN---MPTNKTETPELBPVKAAY 927  
 Qy 925 ILIQDQDSTLYVSPTRPKPKIHOVKMYQVRIOPSIDHNIPTLBAVVGVPQPPSEGP 984  
 Db 928 MVVTSHGVSFKYLNFTASEVTSRVMQHOVQV---SNLQGSFLP-ISLVFLVPLRLQTVI 983  
 Qy 985 THQMSVQMPVPV--PHYEDLELPAAPBCPLFGALFRCPV-- 1024  
 Db 984 WDRPQVTFSENLSTCHTK--EPLPSHSD--FLAEIRKAPVAVNCSTAVCQRIQCDIPLFG 1039  
 Qy 1025 FROEILYQVIGTLELVEIEAS--SMFSLCSSLSISFNSSKPHFLYGSNLSLAQVVMKVQ 1082  
 Db 1040 IQREPAATLKGNLSPMYIKTSHNHLIYSTAAILFNDSVFTLLPQGAFAVRQOTETKVR 1099

QY 1083 VVYEKQMLLYLVLSGIGGLLLLLLIFVLKYGVFFKKRLKEKMEAGRGVPNGIP 1136  
| | | : | | | | | | | : | | | |  
DB 1100 PFEVPNPPLIVGSSVGGLLLALLTAALYKLGFFKKRYKDMMSG-GPPGABP 1152  
| | | | | | | | | | | | | |

## RESULT 9

```

US-08-286-889-3
: Sequence 3, Application US/08286889
: Patent No. 5470953
:
: GENERAL INFORMATION:
: APPLICANT: Gallatin, W. Mich
: APPLICANT: Van der Vieren, Monica
: TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
: NUMBER OF SEQUENCES: 51
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
: STREET: 233 South Wacker Drive, 6300 Sear Tower
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States
: ZIP: 60606-6402
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/286,889
:
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/173,497
: FILING DATE: 23-DEC-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Williams Jr., Joseph A.
: REGISTRATION NUMBER: P38,659
: REFERENCE/DOCKET NUMBER: 27866/32168
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-474-6300
: TELEFAX: 312-474-0448
:
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1153 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: MOLECULE TYPE: protein
:
: US-08-286-889-3

```

Query Match	25.6%	Score 1563	DB 1	Length 1153
Best Local Similarity	34.3%	Pred. No. 1,96-124		
Matches	410	Conservative 210	Mismatches 464	Indels 110
			Gaps	38
QY	6	ITVMAALISGEFFAPASSYNI	DVRCGRSFSPPRAGHFGYRIYQV	-GNGTVGAPBS- 63
		: : : : : :	: : : : : :	: : : : : :
DB	6	LIITLITLTCHEP-----	NLDIENAMTFQ--ENAGCFGSSVQLQCSRIVVAGAPDEI	54
QY	64	--GNSGTSLYYOCQSGTGH	CLPYTLR-GSNYSYKYLGMTLTLPDTSIGLILACDPGLSRTCD	120
		: : : : : :	: : : : : :	: : : : : :
DB	55	VAAANGSLUYQDDYSTGSC	EPRIQLQVPEAVNMSGLSLAAMTSPQLLACGPTVHQCIS	114
QY	121	ONTYISGLCYLFRONLQ	GBMLOGRPQBCIKG---NVDLVFLPDGSSNLSLPDEFQKITL	176
		: : : : : :	: : : : : :	: : : : : :
DB	115	ENTYVKGCLFEGSNLR---	QQPKFPEALRQCPQEBSDIAFLIDGSGSITPHDFRRMK	170
QY	177	DFMDVMKGLNSTYSQ	PAAVGPESTYSKIEPDDSDYVKRKDPALLKHYAKMLLINTYGA	236
		: : : : : :	: : : : : :	: : : : : :
DB	171	BEFVSIVMQLKKSKITL	FSIMQYSBEFRRHFHFFKEQONNPNRPSLVKPIITQLGRTHTATG	230
QY	237	INVAATEVREBELGAR	PDATKYLIIITTGE--ATDSGNIDAKD-----IIRYIIGIGH	289
		: : : : : :	: : : : : :	: : : : : :
DB	231	IRKVURELFNITNGARK	AKAFKLLVVIITGEEKGPDGJEDVILPADREGVIRYIVGVGDA	290

```

OY      290  FOKTESOETHLHKRASKRASEFVKILDOFEKXKOLFTELOKXIYIETSXODLTSFMNEL 349
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      291  FRSKSKQOEINTLTSKRPDRHVQVNNFALKTIQNOJREKFIPIAIEBTQYSSSFHEM 350
OY      350  SSGSISADLSRGHAWGAVGAKWAGGFLDKADODTEIGNEPLTPEVAGLYTVT 409
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      351  SQEGFSAALITNSGRLTSGVSYDMAGVF-LYTSKEKSTFINMTRVDSDDMDVALGYAAA 409
OY      410  WLPERQKTSLASGAPRYQMKRYLLEQEOGGGSHSQVOTIHGTQISYFGEELCGVDV 469
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      410  -ILIRNVQSLVYGAPRYOHIGLVAMER--QNTGMMSSNANVKTOIGAYFGASLCSVDV 466
OY      470  DODETELELIGALFYGEORGGVVFY-----ORQGFEEYSELQGDGCPYLGREGEA 524
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      467  DSNSTDVLILGAPHYTEQTRGGQVSCPLPROGRAMQCDV--LYGEQOQPMGRGAA 524
OY      525  ITALTJINGDGLVDVAVGAPLE--OGAVYIENGHNG-GLSPOSORIEGTQVLSGIQWF 581
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      525  LTVLGDVNGDLTFLVALIGAFGEENRGAVVLFHQTSGSISPSHQRIAGSKSLPRQYF 584
OY      582  GRSHGVKXDLBEGDLADVANGASQMTVLSRPVDMVTILMSBPAPLPHVHEVCSTVS 641
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      585  GQSLSGQDILTMQDLVLTGAGQSHVLLRSQPLRKALIMEFPRVARVFCNQOV 644
OY      642  NKMEGVNITTCFQI-KSLYPOF-QGRVLNVLVTYTLQDGHTRRRELPGRGHELRNI 699
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      645  -KGEABEAVVCLHVQKSTRDLRLBEGIQGVVYTDALDSGRPHSRVAFMETKNSTRQT 703
OY      700  AVT-TSMSCDTSFHPVVCVQDLISPIVNSLNSFMEEBGTPRQDRAQKQDIPILRPSL 758
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      704  QVLGLTQTCETLKLQLPNCIEDPVSPIVLRINSESL--VGTPLPS--AFGN-----LRPVL 753
OY      759  HSEIWEI-----PEKXCGEDKCEALRVSPSARSARALRLTAFASLVELSLSNLEED 813
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      754  AEDAQRLFTALPPEKXCGNDNITCQDDLSTFSPMSLDCLVGSGPREFNVTVIRANGED 813
OY      814  AYWVQLDLHFPFGISFRKVEML---KPHSOIPVSCBELPEBSRLLSRAL---SCNVSP 867
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      814  SYRQVTFEFPFLDLSYKRVSTLQNGRQGRSLRACGS--ASSTVSGALSTGCSINHPI 871
OY      868  FKACHSVALOMFNTLVNNSKQSDVELHANVTCNNEDSLIEDNSATT---ITILYPIN 924
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      872  FPENSEVTFTNITFVDKASIKGNLTLKANVTSENN---MPTNKTEFOLELVPKAAVY 927
OY      925  ILIDQDSDSTLYVSEFTKPKRIHQVKMYQVRIQPSIHNIIFTLBAVVGQPPSESGPI 984
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      928  MWVTSHGVSITKYLNFITASENTSRMQRQYOY--SNUGQSLP-ISLVFLVPALNOTVI 983
OY      985  THQMSVQMEPPV--PCYVEDLERLPDAEPCLPALFRCPV-----1024
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      984  WDRQVTFPEMLSTGCHTK--ERLPSHSD--FLAELRKAPVNCISIAVQRIQCDIPFG 1039
OY      1025  FRQELIVQVIGTELVEGIEAS-SMFSLCSLSLSPMSKHFHYGSNALS-AQVNMKVD 1082
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1040  IQEPEFNATLTKNLEFWDYIKTSHNHLIVSTAEILFNDVSFTLLPFGGAFRSTQETKVE 1099
OY      1083  VVYEKOMLYVVLGIGGLLTLILIFLYLVVGFKNLEKMKMAGAGVPGPIR 1136
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1100  PFEVPPNPLPIVGSVGGLLHLLITALYLTGFFPKQYKDMSEG-GPFGAEP 1152
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
US-08-485-618-3
; Sequence 3, Application US/08485618
; Patent No. 5728533
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: Marshall, O'Toole, Gerstein, Murray & Borun

```

STREET: 233 South Wacker Drive, 6300 Sear Tower  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: United States  
 ZIP: 60606-6402  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/485,618  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/173,497  
 FILING DATE: 23-DEC-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/286,889  
 FILING DATE: 5-AUG-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/362,652  
 FILING DATE: 21-DEC-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Williams Jr., Joseph A.  
 REGISTRATION NUMBER: 38,659  
 REFERENCE/DOCKET NUMBER: 27866/32797  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312-474-6300  
 TELEFAX: 312-474-0448  
 TELEX: 25-3856  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1153 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-485-618-3

Query Match 25.6%; Score 1563; DB 1; Length 1153;  
 Best Local Similarity 34.3%; Pred. No. 1.9e-124;  
 Matches 410; Conservative 210; Mismatches 464; Indels 110; Gaps 38;

QY 6 ITWMAALLSGFFFPASSINILVGRARSPPRAGHFGYRLQV-GNGVIVGABGE- 63  
 DB 6 LILTLALTLCHGF-----NLDTENAMTFQ--ENARFGQSVVQLQSGRVVVGAPQEI 54  
 QY 64 --GNSSTSLVQCGSGTGHCLPVTIR-GSNTSKYLKMTLATDPTDGSILACDPGLSTCTD 120  
 DB 55 VAAQRSGSLVQCDVSTGSCERIRLQVVEAVNMSLGLSLAATYSPQDLACGPTVHTCS 114  
 QY 121 QNTYLSGLCYLFRONLQGPMLQGRPFQFCIKG---NVDLVPLFDGSMSLQDEPQKITL 176  
 DB 115 ENTIVKGLCFPLFGSNLR---QDPQKPEALRGCPQSDIAFLIDSGSIIPDFRRMK 170  
 QY 177 DPKADVWKLSNTSYOPAAVQFSTYKTEBFDSDYVRKQPDALLKHKMLLTNTFGA 236  
 DB 171 EFTSTVMEQLKSKTLPFLSMQYSEFRIHFTPKFQNNPBRSLVKRITQLDGRTHATG 230  
 QY 237 INVATVEFEEBEGARDATKVLIIITDGE--ATDSGNIDAAKD-----IIRYIGIGKH 289  
 DB 231 IRRVRLRFNITGKARNAKFKILVITDGEKFGDPLCYEIVIPADREGVIRVYIGVDA 290  
 QY 290 FQTKESQETLHFKPASKPASEFVKLIDTFEKLKDLFTELQKIYVTEGSKQDLTSPMEL 349  
 DB 291 FRSKSKQBLNTLASKPRPDHVPOVNNFALKITIQNDLREKIFAIESTQSSSSFEHEM 350  
 QY 350 SSSGISADLSRGAAVAVGAKDAGGFLDLKADLQDDTIFIGNEPLTPPEVAGYIGYTVT 409  
 DB 351 SOEGFSAITSNGPLSLSTVGSYDWAQGVF-LYTSKSKSTFINMTRVDSMDMDAIVGYAAA 409  
 QY 410 WLSRQKTSILASGAPRYQMGRVILRFQEPQGGHMSQVQTIHQTOIGSFVGGELCGVDV 469

DB 410 -ILRRNVQSLVAGAPRYQHIGLVAMFR--QNTGMESNANVAGTQIGAFGASLCSVDV 466  
 QY 470 DQGETELLIGAPLFYGEORGRVIFY-----QRRLGFEBSYSELQDGYPLRGGEA 524  
 DB 467 DSGSTDLVLIGAPHYEQTRGGQVSCPLRGGRARMQCDAY--LYGEGQGPWGRGAA 524  
 QY 525 ITALTIDNSGVLAVAVGAPLRE--OGAVYIFNGRHG-GISPDQSORIESTOVLSGIOWF 581  
 DB 525 LTVLGDVNGKLTIDVALGAPGEEDNRGAVLFTGTSGSGISPSHSQILASKLSPRLQYF 584  
 QY 582 GRSIHGVKLEGGDLADVAAGASOMIVLSRPVDMVTLMSSPAPRIVHVECSYSTS 641  
 DB 585 GQSLSGQDLTMDGVLDLTGAGQHVLILASQVYLRKAKALMENPRVAANVEFCNDQV 644  
 QY 642 NRKKEGVNITICFOI-KSLVPQF-QGRVLANTYTLQDGRTRRRLFGGRHELRNT 699  
 DB 645 -KKEAGEVAVCLHVGQSTRDLRREGQISGVTVYDLDLDSGRPHSRVAFNETKSTRQT 703  
 QY 700 AVT-TSMSCIDPSFHPVVCYQDLISPIVNSLMSBEGTPDQRAQGDPIPLRPSL 758  
 DB 704 QVIGLTQTCETLKLQLENCIEDPVSPVLRLNPSL--VGTPLPS--AFGN-----LAPVL 753  
 QY 759 HSETWEI-----PFRKNGEDKCEANLRYSPFAPASRALRLTAFASLYELSLNLEED 813  
 DB 754 AEDAQRLFTLFPFRKNCNDNICQDDLSITFSFMSLDCLVGGPRFRFNTVYTRDGED 813  
 QY 814 AYWVQDLHFPFGLSPFKVEML--KPHSQIPVSCBELPESRLSRAL--SCNVSSPI 867  
 DB 814 SYRTQVTFPFPDLSTRKAVSTLQNSQSRSMRLACES--ASTYVSGALSTSCSINHPI 871  
 QY 868 FKAQSVALLQMMNTLVNSWSDSVELHNAVTCNEDSLLEDSATTT--IPILYIPIN 924  
 DB 872 FPNSEVTFNITPDVSKASLGNKLLKANVTSENN---MPTNKTPEQLELPVKAAY 927  
 QY 925 ILIQDQDSTLYVSPFKGPKIKHQVMQVORLOPSIHNDHNPFLAVVGVPOPPSRGPI 984  
 DB 928 MVVTSHCVSTKYNLNTASNTSRVMQHOYQ---SNIGQSLP-ISLVPLVPRLNQTVI 983  
 QY 985 THQMSVQMBPPV--PCHYEDLERLPDAABPCLPALFRCPV----- 1024  
 DB 984 WDRPQVTFSENLSSTGHTK--ERLPSHD--FLAEKRAVNVCSIAVQRIQCDIPFG 1039  
 QY 1025 FROELVQVITGLTELYGEIRAS-SMFSLCSLSISFNSSGHFHLUGSNAL-AQVVMKV 1082  
 DB 1040 IOEFNAATLKGNLSFPMWYIKTISHNHLIVSTAILFNDSVFTLLPGGAFVRSCOTETKVE 1099  
 QY 1083 VVYEKMVLVYVLSGIGLILLLIFLYKYGVFPFRNKKERKEAGRGVNGIP 1136  
 DB 1100 PFEVNPPLVIGSSVGGILLLITLALVYKGFPRQYKDMSEG-GPGGAP 1152

RESULT 11  
 US-08-362-652-3  
 Sequence 3, Application US/08362652  
 Patent No. 5766850  
 GENERAL INFORMATION:  
 APPLICANT: Gallatin, W. Michael  
 APPLICANT: Van der Vliet, Monica  
 TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit  
 CORRESPONDENCE ADDRESSES:  
 ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun  
 STREET: 233 South Wacker Drive, 6300 Sear Tower  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: United States  
 ZIP: 60606-6402  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/23391
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-362-652-3

```

Query Match 25.6%; Score 1563; DB 1; Length 1153;

Best Local Similarity 34.3%; Pred. No. 1,9e-124;

Matches 410; Conservative 210; Mismatches 464; Indels 110; Gaps 38;

```

6 ITWAMALLSGFFFAFASYSNLDVVGARSPFPRAGRHGVYLOV-GNGVTVGAPGE- 63
6 ILLTALTLGCGF-----NDTENAATFO--ENAKRGOSVVLQSRVVGAPGEI 54
64 --GNSTGSLVQCOSGTGHCIPVTLR-GSNYTSKYLGMTLATDPTDGSIIACDPGLSRTCD 120
55 VANORGSLVQCYSSTGSCPRIRLQVVEAVNMSTGLSLAATTSPPGLACGPTVHQTGS 114
121 QNTYISGLCTLPFQNLQGPMLQGRPGQCICG---NDVLVLPFGDSMSLQDEPQKL 176
115 ENTYVGLGCLFGLFSNLR---QOPQKPEALRGCPQEDSIALFLIDSSGSIIPHDFRMK 170
177 DFKDWKKLSTNSYQPAVQFSTSYKTEPFDSDYVXRKPDALLKHVKMLLTNTFGA 236
171 EFTSTMEQKSKTFLSMQYSEBRRIHTFKERQNNPFRSLVAFITQLGRTHTATG 230
237 INVATEVFRBELGAPDATKVLIIITDGE--ATDSGNIDAKD-----IIRYIIGIKG 289
231 IRAWVELFNITGARKNAFKILVITDSEKFGDPLGYEDVIEADREGVIRVIVIGDA 290
290 FQTKSQEOTLHAKASRPASFFVKILDTFEKLDLFTLEOKKIYVIGSTSKODLSTFMEL 349
291 FSEKSRQELNLTITGAPRDHVFQVNNFELKTIQNLREKIRAIIEGTQGSSESFHEM 350
350 SSSGISADLSRGHAVVGAVGAKDMAGGFLDKXDLDDTFIGNREPLIPEVRAVIGTVT 409
351 SQEGFSAITISNGLSTVSGSYMAGVF-LYTSKESSTIINNTRVDSMNDAYILGAAA 409
410 WLPSSQKTSLLASGAPRYQHMGRVLLFQEPQGGHMSQVOTIGTQIGSYFGEGLGCVDV 469
410 -ILRRRVGSLVAGAPRYQHIGLVAMFR--QNTGMESNANVGTQIGAFGASLGSVDV 466
470 DQDGETELLIGAPLYGEGRCGRVFIY-----QRRLGFEVSELSQGDGYLGRGGA 524
467 DSNGSTDLVIGAPHYEQRGGQVSVCPPLPRQRAWQCDAV--LYGEGQGPWGRGAA 524
525 ITALTINGGLVDVAVGAPLEB--OGAVYIPNGRHG-GLSPQSQRIEETGVLSGIOMF 581
525 LITVLGVDNGLKLDVAIGAPGEEDNRKAVLTFHGTSSGSIPIHSHQSLASGLSPRLQYF 584
582 GRSIHGKDLGEGDGLDVAVGASOMITLSSRPVVDVNTLMSFSPAEIPVHEVCSYSTS 641

```

```

585 GOSLGGQDLTMDGLVDLTVGAQGVLLRSQPVLRVKAIMENPREVANVECDQVY 644
642 NMKKEGVNTTICFOI-KSLYPQF-OGRLVANLTTLQDLGHTTRRGGLPGGRHLEARNI 699
645 -KKEAGEVRCVLHGVKSTRDLRQIQSVVTVYDALDSGRPHSHAVNETKSTRROT 703
700 AVT-TSMSCDPSFHPVVCVDLISFINVLSNFSIMEBGRTPRQRAQKDIPIILRPSL 758
704 QVLGLQTCETLKLQPLNCIEDPVSPIVLRNPSL---VGTLS--AFGN-----LRPVL 753
759 HSEETBEI-----PFRNCGEDKKCEANLRVSSPARSRLRLTAPASLSVEISLSEED 813
754 AEDARLFTLALFPFEKNCNDNDICODDISITFSFMSIDLVLVGGPREFVTVYVRNDGD 813
814 AYVVDLDFHPPLGSRKXEML---KPSQIVSCGELEPESRLISRAL---SCNVSPI 867
814 STRQVTFPPFDLSTRKVTIQQNOSQSRWLACES--ASTEVSGALSKTSCTINHPI 871
868 FRAGHSVALQMMFNTLVNSMGDSVELHANVTCONNEDSDLEBNSATTT---IPILYPIN 924
872 FPNSEVTFNITFDVDSKASLGNKLLKANVISENN---MRTNKTETQLELPVYAVY 927
925 ILIQDQEDSTLYSFTPKPKTHQVKMYQVRIQPSIHDMNIPLEAVVGVPOPESEGI 984
928 MYVTSHVSTKYLINFASENTSRVMQHOYQV---SMLGQSLP-ISTVLVPRILNQTVI 983
985 THOMSVQMPPV--PCYVEDLERLPDAEPCPLGALFRCPVY----- 1024
984 WRPQVTFSENNISSTHTX--EKLPSHSD--FLAEIRKAPVNVCSIAVCORIQCDIPFG 1039
1025 FROELIVQVITGLELVGEIENS-SMFSLSLSISFNSKSHLYXSNASL-AQVVMKYD 1082
1040 IQEENFATLKNLSFPMWYIKTSHNLLIVSTAEILFNDSVFLLPQGAFAVSQETKYE 1099
1083 VYEEKOMLYLVISGIGLLLLILFTVLYKGVFFRRNKEKQMEAGRVPNIGIP 1136
1100 PFEVNPRLPLIVGSSVGLLLALITLALYKLGFFRKQYKDMMSBG-GPGAPF 1152

RESULT 12
US-08-605-672-3
Sequence 3, Application US/08605672
Patent No. 5817515
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994

```

```

ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-605-672-3

Query Match      25.6%; Score 1563; DB 2; Length 1153;
Best Local Similarity 34.3%; Pred. No. 1,9e-124;
Matches 410; Conservative 210; Mismatches 464; Indels 110; Gaps 38;

QY 6 ITTMAALLSGPPFPADASSYNDVGRASFPSPRAGHFGYRLQV-GNGVIYAGPGE-63
DB 6 LITLTLALTLCHGF-----NIDTENAMTFQ--ENARGFQGSVVOLOGSRVYVGAFOEI 54
QY 64 --GNSGTSLVQCCSGTCHCLPYTLR--GSNTSKYLGMTLATDPDGSILACDGLSTCD 120
DB 55 VAANQGRSLVQCCYSTGSCPEIRLQVVEAVNMMSLGLSLATATSPQLLACGFLVHOTCS 114
QY 121 QNTYLSGLCYLFRONLOGPMLQGRPGFOECIKG---NVDLVFLFDGSMLOPDEPOKIL 176
DB 115 ENTYYKGLCELFSGSNLR---QDPQKFPALRGCPQEDSIALILDSGSIIPHDFRMMK 170
QY 177 DFKMDWKKLSNTSYOPAAVOFTSYKTEPDSYVYRKDPDALLKHKMLLTMTFGA 236
DB 171 EFTSTWEOUKSKTLESLMQYSEPRIHFTPEKFPQNNPRLVKNITQLKRTHTATG 230
QY 237 INVAIVFVEBEICAPDPAKTLITTDGR--ATDSGNIDAAD----IIRYIIGIGKA 289
DB 231 IIRVYBELFNTTNGARKNAFKIIVITDGEKFGDPLGEYEVIRBEADREGYIRVYIGVDA 290
QY 290 FOTKESQETLHKFASKPASEFVKILDTFEKLDLFTLELOKIVYIGSTSKQDLSPFMEL 349
DB 291 FBEKSRQELNLTAKRPDPDHVFOVNNFELKTIQNLREKIFALIBSTQSSSFEHEM 350
QY 350 SSGGISADLSRGAHVAVGAGKADWAGFDLADLADDPTEIGNEPLTPRYAGVLYTVT 409
DB 351 SSGGFSALITNSGPPLSTVGSYDMAGVF--LYTSKEXSTFINMTRVDSMDNDAYLGFAA 409
QY 410 WLPDRQKTSILASGAPRYQMGKVLLEFOEPQGGHMSOVOTINGTOIGSYFGSELGVDV 469
DB 410 -ILRRNVOSLVVGAPRYQHIGLVAMFR--QNTGMESNANVKTQIGAYFGASLSCVDV 466
QY 470 DDBGETELLIGAPLFGYBGRGRVFIY-----ORQLGFEYSELQDGGYVLGRGEA 524
DB 467 DSNGSTDLVIGAPHYEBQRGQVSCPLPRQGRAMWQCDAY--LYGEGQGWGRRGAA 524
QY 525 ITALTINGDGLVAVGAPLEE--OGAVYIFNGRHG--GLSPQSPQRIBSTQVLSGIOWF 581
DB 525 LTVLGDVNGDKLDVAIGARBEDNCAVYLPHGTSGSGISPSHSORIASKSLSPRLQYF 584
QY 582 GRSIHGVKDLSEGLADVAVGAESQMTVLSRPVDMVTLMFSFPAEIVPHEVCSYSTS 641
DB 585 GQELSGGQDLTMGLGLVDLTVGAQGHVLLRSQPLRKALIMFRPREVANVEPCNDQV 644
QY 642 NKKKEGNIITICPOI--KSLYPOF--QGLVLANLYTTLQDGHRTRRRLPFGGHEHLRNI 659
DB 645 -KGEKEGEVAVVCLHVQKSTRDLREBQIQSVVYTDALDSGRPSRAVFEYKNSSTRQT 703
QY 700 AVT--TSMSCDTDFSFHFPVAVQDILSPINVLNLSLMEBEGTPRDORAGKDIPIILPSL 758
DB 704 QVGLGLOTGTLKQLQPNCEIDPVSPIVLANLSL---VETPLS--AFGN-----LRPVL 753

```

```

QY 759 HSETWEI-----PEKNCGEKCKEANTLRVSPSPARALRLTAFASLSVELSLNLEED 813
DB 754 AEDAQRLFLALFPFEKNCNDNLCQDDLSTTFMSLDCLVGGPPEFNVTVVRDGED 813
QY 814 AYVWQDLHFPPLGSPKXVEMT---KPHSQIPVSCBELPEESRLSRAL---SCNVSSPI 867
DB 814 SYRTQYTFPPLDLSRYKSTLQNGRSQSRWLACGS--ASSYEVGALKSTSCSINHPI 871
QY 868 FKAGSHVALQMMNTLVNSWGDSEVLHANTVCNNEDSDILENSATTT---IPILYPIN 924
DB 872 FPNSEVTFNITPDVSKASIGKMLLKANVISENN---MPTNTTEFQLEIPLVKAAY 927
QY 925 ILIQDQEDSTLYVFTPKGPKIKHQKMOVRAQPSIHNDIPTLEAVVGVPQPSRGP 984
DB 928 MVTTSQVSTKYTLNFTASERTSRWQHGYOV---SNLQGRSLP--ISLVFLVPLNQTVI 983
QY 985 THQMSVQMBEPV--PCHYEDLERLPDAEPCLEPGALFRCPV----- 1024
DB 984 WDRPQYTFPSNLSSTGHTK--ERLPESHQ--FLAEIRKAPVNVCSIAVQORICODIPFG 1039
QY 1025 FROEILVOYIGTLELVGEIBAS--SMFSLGSSLSISFNSSKHFLYGSNASL--AQVMKVD 1082
DB 1040 IQREFNATLKGNLSPDWYIKTSHNHLLIVSTAILFNDSVFTLLPQGAFAVRSQSTKVE 1099
QY 1083 VVYEKQMLYLYVSGIGLILLLIFLYKVGFEFRKNEKEKAEAGRVNGIP 1136
DB 1100 PFEVNPPLLVGSSVGGILLALLITPALLYKLGFFRQYKDMWSEG--GPGABP 1152

RESULT 13
US-08-482-293A-3
Sequence 3, Application US/08482293A
Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:

```

LENGTH: 1153 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-482-293a-3

Query Match 25.6%; Score 1563; DB 2; Length 1153;  
 Best Local Similarity 34.3%; Pred. No. 1,9e-124;  
 Matches 410; Conservative 210; Mismatches 464; Indels 110; Gaps 38;

QY 6 ITTAMALLISGFPPAPASSYNDVGRGAFSPPRAGHGVYLYQV-GNGVIVAGGE- 63  
 DB 6 LITLALTLGHGF-----NLDTEAMTFQ--ENNRGFGSVVQLQGRVYVGAQOEI 54  
 QY 64 --GNSGSLVQCCSGTGHCLPVTLR-GSNTSKYLGMTLATDTPDGSIIACDGLSRTCD 120  
 DB 55 VAAHQSGSLVQCCVYSTSCSPRIQLQVPEAVNMSLGLSLATTSPPQLLAGCFVHQTC 114  
 QY 121 QNTYLSGLCYLFRONTLQGPMLQGRPGFQECIKG---NVDLVFLFDGMSLQDPDFOKIL 176  
 DB 115 ENTYYVGLGCLFQSNLR-----QQPQKFPFALRGCPQEDSLIATLIDSSGSIITHDPRMK 170  
 QY 177 DEPKDVKKLSNTSYQPAVQFSTYKTEFDSDYKRPDALLKHKMLITNTPGA 236  
 DB 171 EFVSTWEOIKSKSTLFSLMQYSEEFRIHFTFKFQNNPRLVKPITQLLGRTHATG 230  
 QY 237 INVVAEVEPEELGARDATKVLITIDGE--ATDSGNIDAAND---IIRYIIGIKH 289  
 DB 231 IRVVELEFITTNGARKNAKILVITDGKFGDPLQYEVIRPADREGVIRVIGVDA 290  
 QY 290 FQTKESQETLHKRASKPASEFVKILDTFEKIKDLFTLQKKIYVIGTSKQDLPFMEL 349  
 DB 291 FPEKESQELANTLASKPRPHVFOVNNFEALKTIQNGLRKIKALIBETQSSSPEHEM 350  
 QY 350 SSSGISADLSRGNAVVGAKQWAGGFLLDKADLDQDTFIGNEPITREVRAGLYGTVT 409  
 DB 351 SQRFSAATISNGPLSLTVSGSYMAGVF--LYTSKESKTFINMTRVSDMNDVLYGAAA 409  
 QY 410 WLPSSQKTSLLASGAPRYOMGRVLLFQEPQGGHMSQVQTINGTOISGAFGBELGVDV 469  
 DB 410 -ILRNKVGSLVIGAPRYQHIGLVAMFR--QNTGMESNANVNGTQIGAFGASLGSVDV 466  
 QY 470 DQDETELLIGAPLFYBQGRGRVFY-----QRRLGFEVSEIQLGDPYLGFRGA 524  
 DB 467 DSNKSDVLVIGAPHYEQTRGQVSCPLPRGQRARWQCDV--LYBEGQGWGRGA 524  
 QY 525 ITALTIDINGDLVDVAVAPLEP--QGVYITFNGRHG-GLSPQSORICTQVLSGIQWF 581  
 DB 525 LTVLIGVNGDKLTDVAIGAPGEENRGAVLLFHTSGSGISPSHSQRLASPLQYF 584  
 QY 582 GRSHVQKDLGEGGLADVAVAGSOMTVLSRPVDMVTLMSPRAIIPVHEVCSTSTS 641  
 DB 585 GQSLSGQDITMGVLVDLVGAQGHVLLLSQPLRKALMEINPREVANVECDQV 644  
 QY 642 NKMKGVNITICFOI--KSLYPOF--QGRLVANLTVYTLQDGHTRRRGLFGCHHELARNI 699  
 DB 645 -KCKRGEAVVCLAHVQKSTRDLRREGIQSVVYTDLALDGRHSRAVFMETNSRRQT 703  
 QY 700 AVT-TSMSCDTDFHFHPVCVQDILSPINVLNLSLWEEESTPRDQAGKDIPILRPSL 758  
 DB 704 QVGLQTCETKLQIQLPNCIEDPVSPIVRLNFSL--VETPLS--AFGN-----LRPVL 753  
 QY 759 HSETWEL-----PEKKGCDKXCEANLRVSPPARARALRUFASLSYLSLNEED 813  
 DB 754 ABDAQRIFLALFPPEKCGANDNIQQDLSITFSMSLDCVLVGGPREFNTVTVRNDGED 813  
 QY 814 AYVWQDLHPPGLSPFKVEML--KPHSQIPVSCBELPRESRLISRAL--SCNVSSPI 867  
 DB 814 SYRTQVTFPPFDLSLTKVSTLQNGRSQRWRLACES--ASSTVSGALSTGCSINHPI 871  
 QY 868 FKAGHSVALQOMFNTLVNWSGDSVBLHANVTCCNEDSDLLLEDN SATTI--IPILYPIN 924

DB 872 PRENSEVETNITFDVDSKASLGNKLLKANVTSENN---MBRTNTEFOLELPVKYAVY 927  
 QY 925 IILIQDEDESTLYVFTPKGPKLHOVKMYQVRIQPSIHDHNIPTLEAVGVFPQPESEPI 984  
 DB 928 MYVTSHGVSITKYNITFASSENTSRVMOHQYV--SNLQGRSLP-ISLVLVVPRLANQYVI 983  
 QY 985 THQMSVQMBPV--PCHYDELERLPDAAPCLPGLFRCPVV----- 1024  
 DB 984 WRPQVTFEENISSTCHTK--ERLPESHSD--FLAELRKAPVNVNCSIAVCRIQCDIPFG 1039  
 QY 1025 FROELIVQVITGLVELGEIEAS-SMPSLCSLSISPSNKHHLVGSNASL-AQVVMKTD 1082  
 DB 1040 IOEEFNATLKGMSLSPDMYIKTSHNMLIVSTAELIFNDSVFLLPQOGAFVRSQETTKYE 1099  
 QY 1083 VYTERKQMLVYVLSGIGLLLLITFLVLYKVGFPKRNKEMWAGRGVNPNGIP 1136  
 DB 1100 PREVPNPFLVIGSSVGGLLLLITALLYKLGFFKRYQKDMMSG-GRPGAR 1152

RESULT 14  
 US-08-943-363-3  
 Sequence 3, Application US/08943363  
 Patent No. 5837478  
 GENERAL INFORMATION:  
 APPLICANT: Gallatin, W. Michael  
 APPLICANT: Van der Vieren, Monica  
 TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit  
 NUMBER OF SEQUENCES: 114  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Marshall, O'Toole, Gerstelein, Murray & Borum  
 STREET: 233 South Wacker Drive, 6300 Sear Tower  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: United States  
 ZIP: 60606-6402  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/943,363  
 FILING DATE:  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/173,497  
 FILING DATE: 23-DEC-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/286,889  
 FILING DATE: 5-AUG-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/362,652  
 FILING DATE: 21-DEC-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Williams Jr., Joseph A.  
 REGISTRATION NUMBER: 38,659  
 REFERENCE/DOCKET NUMBER: 27866/32684  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312-474-6300  
 TELEFAX: 312-474-0448  
 TELEX: 25-3856  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1153 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-943-363-3  
 Query Match 25.6%; Score 1563; DB 2; Length 1153;  
 Best Local Similarity 34.3%; Pred. No. 1,9e-124;  
 Matches 410; Conservative 210; Mismatches 464; Indels 110; Gaps 38;



```

QY 6 ITWAMALISGFFFPADASSYNLDVRGARSFSPRAGRHFYVLOV-GNGVIVGABGE- 63
DB 6 LILFALTALCHGF-----NLDTENAMTFQ--ENARGGQSVVLOQSGRVVVGABGEI 54
QY 64 --GNSGSLVQCGSGTGCHCLPVTLR-GSNYSKYLGNTLATDPTDGSILACDPLGSRCTD 120
DB 55 VAANQSGSLVQCGSVGSGCEPIRLQVPEAVNMISLGSLAATTSPPQLACGPTVHQTS 114
QY 121 QNTYLSGLCTLFRONLQGPMLQGRPGFQECIKG---NVDLVLFPDGSMSLQDPDEQKIL 176
DB 115 ENTYYKICLFLFSGSNLR-----QQPKPEALRGCPQEDSDIAFLIDSGSIIIPHDFRMK 170
QY 177 DFMKWKKLKSNYSYQPAVOFSYKTEPDPFSDYVRKOPDALLKVKHMLLTNTFCA 236
DB 171 EFVSTVMEQKSKTFLSMQYSEEFRIHFTFKFQNNPNRSLVKTITDGLGTHRTATG 230
QY 237 INVATEVFEELGARPDPATKVLIIITDGE--ATDSGNIDAAD-----IIRYIIGIKH 289
DB 231 IRKVRRELFINITNGARKNAFKILVITDGEKPGDPLGEDVIRPADREGVIRYIVGDA 290
QY 290 FQTKESQETLHKRASPASEFVKILDTFEKLDLFTLEOKKIYIEGTSKODLTSFMEL 349
DB 291 FRESKSHQELNTIASKEPRDHVFQVNNFELKTIQNLREKIPAIEGTQSSSSFEHEM 350
QY 350 SSSGISADLSRGHNAVANGAKMAGFLLDKADLDDPTIGNEPLTPEVRAGLYGTVT 409
DB 351 SQGFSAITISNGPLSTVGSYDMAGVF-LYTSKESKSTFIMNTRVSDMNDALGYAAA 409
QY 410 WLPSPKTSILASGAPRYOHMGVRLFOEPQGGHMSOVOTIHGTQISGYFGEELGVNDV 469
DB 410 -IILRRVQSLVLAGPRYOHIGLVAMFR--QNTGMESNANVGTQIGAFGASLCSVDV 466
QY 470 DQDGETELLIGAPLFYGEORGRVFITY-----QRQLGFEVSELOQDPGYLGRGEA 524
DB 467 DSNGSTDLVILIGAPHYEQTRGGQVSVCP-PRGGRAMQCDV--LVGEGQGPWGRFGAA 524
QY 525 ITALTDINGGLVDVANGAPLEB--QCAVYIFNGRHG-GLSPQSGQIEGTQVLSGQWF 581
DB 525 LTVLGDVNGKLDVAGAPGEEDNRGAVYLFHGTSGSGISPSHSQISIASKSPRLQYF 584
QY 582 GRSHGVKDEGDLAVVAGASQOMVLSSRPVVDVNTLMSFSPARIVHEVCSSTS 641
DB 585 GQSLSGQDLDMDGLVDLVGAGQSHVLLRSQVLAKEFNRVARVARECNDQV 644
QY 642 NKKEGVNITICFOI-KSLYPOF-QGRVANTLTYTLOLDGRTERRGLFGGRHELEARNI 699
DB 645 -KKGKAGEVAVCLHVQSTRDLREGOIGSVYTYDLDLDSGRPHSRVAFHETKNSRQF 703
QY 700 AVT-TSMSCITDFSGHFVQVODLISPIVNSLNSFMEBEGTPRDQAOQKDIPILRSL 758
DB 704 QVGLTQTCETLKLQLPNCIEDPVSPVILRLNFSL--VGTPLS--AFGN-----LAPVL 753
QY 759 HSEHWEI-----PEKKCGEDKCKEALRYSPSPARSARALRLTAPALSVELSISNEED 813
DB 754 AEDARQRLFTLFPPEKCGANDNICQDDLSTFSPMSIDCLVGGPREFNVTYVRANGED 813
QY 814 AYWVQDLHFPFGISFPRKVMEL---KPHSOIPVSCBELPESRLLSRAL---SGNVSP 867
DB 814 SYRTQVTFPFLDLSYKVKSTLQNGRQSRMLACES--ASSTVSGALSTSGSINHPI 871
QY 868 PKAGHVALQMMFNTLVNSSMGDSVELHNAVYTCNNEEDSLLIEDNSATTT---IPILYPIN 924
DB 872 FPNSEVTEFNTFTEVDSKASLIGNKLILKANVTSENN---MPRTNKTPEOLETPEVKAAY 927
QY 925 ILIQDQSDSTLYVSFTEPKGIHQVKMYOVRLOPSTHDNIPTLEAVVGPQPSGPI 964
DB 928 KVVYTSHGVSCTKLNTFASENTSRYWQHQYOV---SNLQGRSLP-ISLVFLVPRALNQTVI 983
QY 985 THQMSVQMEBPV--PCHYEDLERLDAABPCLPGLFRCPV-----1024
DB 984 WDRQVYTFSENLSSTGHTK--ERLPSHD--FLAELAKAPVYVNSIAVQGRICQDIPFPG 1039

```

```

QY 1025 PROELIVQVIGTELVEIGEIAS--SMFSLCSLSISFNSGHFLYGSNALS-AQVWVKVD 1082
DB 1040 IOEFNATLKNLSFDMYIKTSHNHLIVSTAILPRDSYFTLLPGGAVRQOTERVE 1099
QY 1083 VYREKQMLYLYLSGIGLILLLIFLYVLYKGFPRKRLKRNKAGEGVENGIP 1136
DB 1100 PFEVPMPLPLIVGSSVQGLLLALITLALYKLGFFPKQYQYDMMSSEG-GPGABP 1152

RESULT 15
US-09-193-043-3
; Sequence 3, Application US/09193043
; Patent No. 6251395
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vliet, Monica
; TITLE OF INVENTION: No. 6251395el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/193, 043
; CURRENT FILING DATE: 1998-11-16
; EARLIER APPLICATION NUMBER: 08/173,497
; EARLIER FILING DATE: 1993-12-23
; EARLIER APPLICATION NUMBER: 08/286,889
; EARLIER FILING DATE: 1994-08-05
; EARLIER APPLICATION NUMBER: 08/362,652
; EARLIER FILING DATE: 1994-12-21
; EARLIER APPLICATION NUMBER: 08/943,363
; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-193-043-3

Query Match      25.6%; Score 1563; DB 3; Length 1153;
Best Local Similarity 34.3%; Pred. No. 1,9e-124;
Matches 410; Conservative 210; Mismatches 464; Indels 110; Gaps 38;

QY 6 ITWAMALISGFFFPADASSYNLDVRGARSFSPRAGRHFYVLOV-GNGVIVGABGE- 63
DB 6 LILFALTALCHGF-----NLDTENAMTFQ--ENARGGQSVVLOQSGRVVVGABGEI 54
QY 64 --GNSGSLVQCGSGTGCHCLPVTLR-GSNYSKYLGNTLATDPTDGSILACDPLGSRCTD 120
DB 55 VAANQSGSLVQCGSVGSGCEPIRLQVPEAVNMISLGSLAATTSPPQLACGPTVHQTS 114
QY 121 QNTYLSGLCTLFRONLQGPMLQGRPGFQECIKG---NVDLVLFPDGSMSLQDPDEQKIL 176
DB 115 ENTYYKICLFLFSGSNLR-----QQPKPEALRGCPQEDSDIAFLIDSGSIIIPHDFRMK 170
QY 177 DFMKWKKLKSNYSYQPAVOFSYKTEPDPFSDYVRKOPDALLKVKHMLLTNTFCA 236
DB 171 EFVSTVMEQKSKTFLSMQYSEEFRIHFTFKFQNNPNRSLVKTITDGLGTHRTATG 230
QY 237 INVATEVFEELGARPDPATKVLIIITDGE--ATDSGNIDAAD-----IIRYIIGIKH 289
DB 231 IRKVRRELFINITNGARKNAFKILVITDGEKPGDPLGEDVIRPADREGVIRYIVGDA 290
QY 290 FQTKESQETLHKRASPASEFVKILDTFEKLDLFTLEOKKIYIEGTSKODLTSFMEL 349
DB 291 FRESKSHQELNTIASKEPRDHVFQVNNFELKTIQNLREKIPAIEGTQSSSSFEHEM 350
QY 350 SSSGISADLSRGHNAVANGAKMAGFLLDKADLDDPTIGNEPLTPEVRAGLYGTVT 409
DB 351 SQGFSAITISNGPLSTVGSYDMAGVF-LYTSKESKSTFIMNTRVSDMNDALGYAAA 409
QY 410 WLPSPKTSILASGAPRYOHMGVRLFOEPQGGHMSOVOTIHGTQISGYFGEELGVNDV 469
DB 410 -IILRRVQSLVLAGPRYOHIGLVAMFR--QNTGMESNANVGTQIGAFGASLCSVDV 466
QY 470 DQDGETELLIGAPLFYGEORGRVFITY-----QRQLGFEVSELOQDPGYLGRGEA 524

```

Dh	467	DSN\$TDLVLGAHHYIEQTRGGGVSVLPRLRGQARAOCDV--LYEEOQPMGRFPA	524
Qy	525	ITALTDINGDLVAVAVAGAPLEE--QGAVYIENGHRG--GLSPQPSQRIEQTQVLSIQMF	581
Dh	525	LTVAGDVVGDKLTVAGAPGEBIDNRGAUVLFHGTSGSGISPSHQRIAGSKLSPRLQYF	584
Qy	582	GRSLHGVKDEBGDGLAVAVAGAESMTVLSRPPVDMVTLMSFSAELPVHEVECSYSTS	641
Dh	585	QOSISGGDLMDEGLVLDLTVAGQGVHLLRLSQPVLRYAIMEFNRBYARVVFECNDQV	644
Qy	642	NKMEGVITTCFOI--KSLYPOF--QGRVLAMITYLLODGRTRRGFLPGGRHELRNI	699
Dh	645	-KGEAGEVRVCLAVQKSTRDLREBGQIQSVTTDLDLDSGRPHSRAYFNETKSTRQT	703
Qy	700	AVT--TSMSCDPSFHFPVQVODLSPINVSINFSIMEEBGTPRDQRAQKDIPLLRSJ	758
Dh	704	QVLGLTQCETKLQLPNCIEDPVSPIVLRNFSI--VGRPLS--AFGN-----LREVL	753
Qy	759	HS\$TWEI-----PEPKNGEDKCEANLRVSPSPRSALMLTAPASISVELSLSNLEED	813
Dh	754	AEDAQRLPETAPEPKKNGNDNIQDDLSITFSFMSJDLVAVGGREPNVTVYVANDSD	813
Qy	814	AYWVOLDHPPEG\$SFRKVEML--KPHSQIPVSCCELPBESRLLSRAL--SCNVSPFI	867
Dh	814	SYRQVTPFFPLD\$SYKRVSTLQNRSGRSWRACES--ASTEV\$GALKXSTCSINHPI	871
Qy	868	EKA\$H\$VALQMMFNTLVN\$SWGDSVELHANYTNNED\$DLEDSATYI--IPLYEIN	924
Dh	872	FPENSEVTFNITPVD\$KASLGKLLKANYTSENN--MPTKTEFOLELPKAVAV	927
Qy	925	ILLODQEBSTLYVSTFPKPKIHQVKNYQVRIG\$SHDHNIPTLEAVVGPQPPSEBPI	984
Dh	928	MVAVTSHGVSTYKLNFT\$ASENTSRVWQHOYV--SNLQORSLP--ISLFLVPLRLQTVI	983
Qy	985	THQ\$VQMEPEV--PCHYEDLERLEDAEPCLPGL\$FRCPVY-----1024	
Dh	984	WDRQVYTSSEML\$STCHTK--ERLP\$HD--PLAELRA\$PVNCSIANCQRIQCDIPFG	1039
Qy	1025	FRQ\$ELLVONITLELVEGEI\$AS-SMFSIC\$SISISFN\$SKPHLYGN\$AST-AQVWYKD	1082
Dh	1040	IQ\$EFNATKLNLSF\$DWYIKT\$SHNLLIV\$TAEILFND\$SVFTLPLGQAFVRSQETKVE	1099
Qy	1083	VV\$EKOMLYLV\$SGIIGLLLLLLLYLVYVGFPRKRLK\$KMEAGREVPKGP	1136
Dh	1100	PP\$VNPRLPLV\$G\$VGGLLLLALIT\$ALIT\$ALYKLG\$FKRQYKQ\$M\$SG-GPQAP	1152

Search completed! August 30, 2005, 11:53:02  
Job time : 51 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: August 29, 2005, 19:15:58 ; Search time 29 Seconds

(without alignments)  
3681.849 Million cell updates/sec

Title: US-09-945-265-2

Perfect score: 6106

Sequence: 1 MKDSCITYMNAALSGFFRF.....DPGLKPLHEKDSGSGGKD 1170

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6098	99.9	1170	2	SO3308
2	4343.5	71.1	1163	2	156126
3	1563	25.6	1153	1	RWHUUB
4	1526.5	25.0	1163	1	RWHUUC
5	1514.5	24.8	1153	2	S00551
6	1114.5	18.3	1151	2	A45226
7	1112.5	18.2	1180	2	A35854
8	1012.5	16.6	1170	2	A45914
9	985	16.1	1181	2	A33998
10	976.5	16.0	1179	2	A53213
11	959	15.7	1178	2	S44142
12	678.5	11.1	1035	2	158409
13	633	10.4	1039	2	A41131
14	619.5	10.1	1038	2	S06046
15	588	9.6	1041	2	T31437
16	557.5	9.1	1041	2	T31437
17	546	8.9	1137	2	JC5950
18	536.5	8.8	1051	2	A35761
19	536.5	8.8	1051	2	A40021
20	530	8.7	1049	2	A27079
21	522	8.5	1053	2	155534
22	521.5	8.5	1054	2	JC7294
23	508.5	8.3	1106	2	S38783
24	487	8.0	1053	2	S44250
25	480.5	7.9	1037	2	A60163
26	478	7.8	1039	2	A34269
27	476.5	7.8	1394	2	A29637
28	473.5	7.8	1146	2	S40311
29	467.5	7.7	1044	2	S16516

30	463.5	7.6	1073	2	B36429	integrin alpha-6 c
31	462.5	7.6	1072	2	A38457	integrin alpha-6 c
32	460	7.5	1034	2	A36108	integrin alpha-V c
33	451.5	7.4	1226	2	S54824	F54F2.1 protein -
34	449.5	7.4	1091	2	A41543	integrin alpha-6 c
35	437.5	7.2	1115	2	T09433	integrin alpha cha
36	436.5	7.1	1044	2	T10050	integrin alpha-v c
37	434.5	7.1	1045	2	S60571	integrin alpha v c
38	433.5	7.1	1115	2	T09403	integrin alpha cha
39	419	6.9	764	2	A136916	integrin alpha cha
40	408	6.7	1048	2	A27421	integrin alpha-5 c
41	384.5	6.3	1139	2	S28277	hypothetical prote
42	343	5.6	1086	2	T18523	integrin alpha cha
43	296.5	4.9	604	2	T136917	glycoprotein IId -
44	251.5	4.1	272	2	A55348	integrin alpha-1 -
45	244	4.0	3124	2	A40020	collagen alpha 1(X

## ALIGNMENTS

RESULT 1  
S03308  
cell surface glycoprotein CD11a precursor - human  
N:Alternate names: leukocyte adhesion glycoprotein LFA-1 alpha chain; leukocyte function  
C:Species: Homo sapiens (man)  
C:Date: 28-Feb-1990 #sequence revision 28-Feb-1990 #text\_change 09-Jul-2004  
C:Accession: S03308; A47458; A47565; A48759; S36044  
R:Larsen, R.S.; Corbi, A.L.; Berman, L.; Springer, T.  
J Cell Biol. 108, 703-712, 1989  
A:Title: Primary structure of the leukocyte function-associated molecule-1 alpha subunit  
A:Reference number: S03308; MUID:89139587; PMID:2537322  
A:Accession: S03308  
A:Molecule type: mRNA  
A:Residues: 1-1170 <LFA>  
A:Cross-references: UNIPROT:P20701; UNIPROT:Q9UBC8; EMBL:Y00796; NID:G31421; P1DN:CAA687-  
A:Note: part of this sequence was confirmed by protein sequencing  
R:Corriveau, R.D.; Gollahan, K.A.; Hickey, D.D.  
Proc. Natl. Acad. Sci. U.S.A. 90, 4221-4225, 1993  
A:Title: Description of the leukocyte function-associated antigen 1 (LFA-1 or CD11a) pro-  
A:Reference number: A47458; MUID:93248261; PMID:8097887  
A:Accession: A47458  
A:Molecule type: DNA  
A:Residues: 1-20 <COR>  
A:Note: sequence extracted from NCBI backbone (NCBIN:130862, NCBI:130863)  
R:Shelley, C.S.; Farokhzad, O.C.; Arnout, M.A.  
Proc. Natl. Acad. Sci. U.S.A. 90, 5364-5368, 1993  
A:Title: Identification of cell-specific and developmentally regulated nuclear factors ti  
A:Reference number: A47565; MUID:93281759; PMID:8099450  
A:Accession: A47565  
A:Molecule type: DNA  
A:Residues: 1-20 <SHS>  
A:Cross-references: GB:M95609  
R:Nueda, A.; Lopez-Cabrera, M.; Vara, A.; Corbi, A.L.  
J. Biol. Chem. 268, 19305-19311, 1993  
A:Title: Characterization of the CD11a (alphaL, LFA-1alpha) integrin gene promoter.  
A:Reference number: A48759; MUID:93374910; PMID:8103515  
A:Accession: A48759  
A:Molecule type: DNA  
A:Residues: 1-20 <NUE>  
A:Cross-references: EMBL:Z22804; NID:G311405; P1DN:CAA80461.1; P1D:G311406  
C:Genetics:  
A:Gene: GDB:ITGAL; CD11A  
A:Cross-references: GDB:119757; OMIM:153370  
A:Map position: 16p11.2-16p11.2  
C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homo  
C:Keywords: cell adhesion; cytoskeleton; glycoprotein; heterodimer; surface antigen; trar  
F:1-25/Domain: signal sequence #status predicted <SIG>  
F:26-110/Product: leukocyte adhesion glycoprotein LFA-1 alpha chain #status predicted <I  
F:154-317/Domain: von Willebrand factor type A repeat homology <VMA2>

Query Match 99.9%; Score 6098; DB 2; Length 1170;  
Best Local Similarity 99.9%; Pred. No. 0;

Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
Oy	1	MDKSCITVMAWALLSGFFFPAPASSYNLDVGAASFPPRAGRHHGVVLQVNGVITGA	60
Db	1	MDKSCITVMAWALLSGFFFPAPASSYNLDVGAASFPPRAGRHHGVVLQVNGVITGA	60
Oy	61	PGEGNSTSLYQCSGSGTGHCLPVTLRGSAVTSKYLGMTLATDPTDGSILACD PGLSRTCD	120
Db	61	PGEGNSTSLYQCSGSGTGHCLPVTLRGSAVTSKYLGMTLATDPTDGSILACD PGLSRTCD	120
Oy	121	QNTYLSGLCTYFRQMLQGPMLQGRPFQECIKGNVDLYFLFDGSGSLDPDEFQKLDPMK	180
Db	121	QNTYLSGLCTYFRQMLQGPMLQGRPFQECIKGNVDLYFLFDGSGSLDPDEFQKLDPMK	180
Oy	181	DVMKSLNSTYQFAVQSTSKTEFDSYVKRDPALLKHVGMMLLNTTGAIVYV	240
Db	181	DVMKSLNSTYQFAVQSTSKTEFDSYVKRDPALLKHVGMMLLNTTGAIVYV	240
Oy	241	ATEVFRRELGARPDATKVLIIITDGEATDSGNIDAADIIIRYIIGIGHFQTKESQETLH	300
Db	241	ATEVFRRELGARPDATKVLIIITDGEATDSGNIDAADIIIRYIIGIGHFQTKESQETLH	300
Oy	301	KPASKPASEFYKILDTFEKLKDLFTELQKTYVIEGTSKODLTSFNMELSSSGISADLSR	360
Db	301	KPASKPASEFYKILDTFEKLKDLFTELQKTYVIEGTSKODLTSFNMELSSSGISADLSR	360
Oy	361	GHAUVGAAGAKOMAGFLDLKADLDDPTFIGNEPITPEVRAGYLGTYTWMPSRQKTSLL	420
Db	361	GHAUVGAAGAKOMAGFLDLKADLDDPTFIGNEPITPEVRAGYLGTYTWMPSRQKTSLL	420
Oy	421	ASGAPRYOMGRVLLFOEPQGGHMSQVQTIHGTOIGSYFGGELCGVVDQDGEITELLI	480
Db	421	ASGAPRYOMGRVLLFOEPQGGHMSQVQTIHGTOIGSYFGGELCGVVDQDGEITELLI	480
Oy	481	GAPLFYQGRGGRVFIYQRRQLGFEEVSELQDPCGYLGRFGBAITALTINDGGLDVVA	540
Db	481	GAPLFYQGRGGRVFIYQRRQLGFEEVSELQDPCGYLGRFGBAITALTINDGGLDVVA	540
Oy	541	VGAPLEEGGAVYIFNGRHGSLSPQPSQRIEGTVLSGIQWFGRSIHGVKDLBGDLAVVA	600
Db	541	VGAPLEEGGAVYIFNGRHGSLSPQPSQRIEGTVLSGIQWFGRSIHGVKDLBGDLAVVA	600
Oy	601	VGASQMTVLSRPVVDVTLMSFSPARIPVHEVCSYSTSNKMGENVITICFOIKSLY	660
Db	601	VGASQMTVLSRPVVDVTLMSFSPARIPVHEVCSYSTSNKMGENVITICFOIKSLY	660
Oy	661	POFQGRVLAANTYITQLDGHRTRRGLFPGGRHELRNIAYTSSMCTDPSFHFVVCVD	720
Db	661	POFQGRVLAANTYITQLDGHRTRRGLFPGGRHELRNIAYTSSMCTDPSFHFVVCVD	720
Oy	721	LISPIVNSLWMEEGTTPRDQRAQGDIPILRPSLSHSETWEIPEKNGCEBCKKCAN	780
Db	721	LISPIVNSLWMEEGTTPRDQRAQGDIPILRPSLSHSETWEIPEKNGCEBCKKCAN	780
Oy	781	LRVSSPASPALRLTAFASSVSELSSLNEBEDAWVOLDLHFPGLGFRKEMLKPHSQ	840
Db	781	LRVSSPASPALRLTAFASSVSELSSLNEBEDAWVOLDLHFPGLGFRKEMLKPHSQ	840
Oy	841	IPVSCBEPPEBSRLISRALSCNVSSPIFKAGHSVALQMMFNTLVNNSGSDSVELHANTYC	900
Db	841	IPVSCBEPPEBSRLISRALSCNVSSPIFKAGHSVALQMMFNTLVNNSGSDSVELHANTYC	900
Oy	901	NNEDSDLEDNSATTIIPILYPINLLIDQDSDSTLYVFTPKGPKIHQVKHMYQVRLOPS	960
Db	901	NNEDSDLEDNSATTIIPILYPINLLIDQDSDSTLYVFTPKGPKIHQVKHMYQVRLOPS	960
Oy	961	IHDHNIPTLEAVVGPQPSSEGPITHQWSVQMEPPVPCHEYEDLELPAABECPLGALFR	1020
Db	961	IHDHNIPTLEAVVGPQPSSEGPITHQWSVQMEPPVPCHEYEDLELPAABECPLGALFR	1020
Oy	1021	CPVVFROEILVQVIGTLELVEIEIASSMFSLCSSLSISFNSSKHFHLVGSNASTLAQVVMK	1080
Db	1021	CPVVFROEILVQVIGTLELVEIEIASSMFSLCSSLSISFNSSKHFHLVGSNASTLAQVVMK	1080

Oy	1081	VDVYERQMTLYLVLSIGIGLLLLIFIVLYKVFERNLKEKMEAGRGVPNGIPAEBS	1140
Db	1081	VDVYERQMTLYLVLSIGIGLLLLIFIVLYKVFERNLKEKMEAGRGVPNGIPAEBS	1140
Oy	1141	EQLASQGEADPGCLKPLHEKDESGGGKD	1170
Db	1141	EQLASQGEADPGCLKPLHEKDESGGGKD	1170
RESULT 2			
156126			
Lymphocyte function-associated molecule-1- $\alpha$ - mouse			
C:Species: Mus musculus (house mouse)			
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004			
C:Accession: 156126			
R:Kaufman, Y.; Tseng, E.; Springer, T.A.			
J: Immunol. 147, 369-374, 1991			
A:Title: Cloning of the murine lymphocyte function-associated molecule-1 $\alpha$ -subunit ar			
A:Reference number: 156126; MUID:91268576; PMID:2051027			
A:Accession: 156126			
A:Status: preliminary; translated from GB/EMBL/DBJ			
A:Molecule type: mRNA			
A:Repeats: 1-1163 <RES>			
A:Cross-references: UNIPROT:P24063; GB:M60778; NID:9198785; PIDN:AAA39426.1; PID:9198786			
C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homol			
F:151-315/Domain: von Willebrand factor type A repeat homology <VMA>			
Query Match			
Best Local Similarity 72.1%; Score 4343.5; DB 2; Length 1163;			
Query 13 LLSGFFPAPASSYNLDVGAASFPPRAGRHHGVVLQVNGVITGAPEGNSTGSLYQ			
Db	11	LLLSGLQFAWMSYNLDTTRPTQSEFL-AQAGRHFQYQVLTIEDGVVGAPEGNDTGGLYH	69
Oy	73	COSGTGCLPVTLRGSAVTSKYLGMTLATDPTDGSILACD PGLSRTCDONTYLSGLCYLF	132
Db	70	CRISSEFCQPSVLSHSGNHTSKYLGMTLATDAKSLACD PGLSRTCDQNTYLSGLCYLF	129
Oy	133	RQNLQGMLOGRPFQECIKGNVDLYFLFDGSGSLQDPEFOKILDPFKMDVMKLSNYSYQ	192
Db	130	PQSLQGMLOGRPFQECIKGNVDLYFLFDGSGSLQDPEFOKILDPFKMDVMKLSNYSYQ	189
Oy	193	FAAVQSTSKTEFDSYVKR-KDPDALLKHVGMMLLNTTGAIVYVATEVFRRELGA	251
Db	190	FAAVQSTSKTEFDSYVKR-KDPDALLKHVGMMLLNTTGAIVYVATEVFRRELGA	249
Oy	252	RPDATKVLIIITDGEATDSGNIDAADIIIRYIIGIGHFQTKESQETLHFKPASPASEFV	311
Db	250	RPDATKVLIIITDGEATDSGNIDAADIIIRYIIGIGHFQTKESQETLHFKPASPASEFV	309
Oy	312	KILDTFEKLKDLFTELQKTYVIEGTSKODLTSFNMELSSSGISADLSRGAHVAVGAYGAK	371
Db	310	KILDTFEKLKDLFTELQKTYVIEGTSKODLTSFNMELSSSGISADLSRGAHVAVGAYGAK	369
Oy	372	DWAGGFIDLKADLDDPTFIGNEPITPEVRAGYLGTYTWMPSRQKTSLLASGAPRYOMG	431
Db	370	DWAGGFIDLKADLDDPTFIGNEPITPEVRAGYLGTYTWMPSRQKTSLLASGAPRYOMG	429
Oy	432	RVLVLFQEPQGGHMSQVQTIHGTOIGSYFGGELCGVVDQDGEITELLI GAPLFYQGRG	491
Db	430	RVLVLFQEPQGGHMSQVQTIHGTOIGSYFGGELCGVVDQDGEITELLI GAPLFYQGRG	489
Oy	492	GRVFTYQRRQSLPFAMVSELQDPCGYLGRFGAATALTINDGRLTVAVAGAPLEEGAV	551
Db	490	GRVFTYQRRQSLPFAMVSELQDPCGYLGRFGAATALTINDGRLTVAVAGAPLEEGAV	549
Oy	552	YIFNGRHGSLSPQPSQRIEGTVLSGIQWFGRSIHGVKDLBGDLAVVAGASQMTVLS	611
Db	550	YIFNGRHGSLSPQPSQRIEGTVLSGIQWFGRSIHGVKDLBGDLAVVAGASQMTVLS	609

QY 612 SRPVDMNTLMSPFAETPVHEVECSYSTSNKMGKGNVITICFOIKSLYPOQGRVAVNL 671  
 DB 610 SRPVDMNTLMSPFAETPVHEVECSYSTSNKMGKGNVITICFOIKSLYPOQGRVAVNL 669  
 QY 672 TTTTLDGHRTRRRLGFPGRHLEARNIAVTTSMGCTPFSFFHPVPCVODLSPIVANSNF 731  
 DB 670 SYTLDDGHRTRRRLGFPGRHLEARNIAVTTSMGCTPFSFFHPVPCVODLSPIVANSNF 729  
 QY 732 SLMEEGTPRDRQAQKDIPIILRPSLSHSETWIPEKXNGGDKKCEANLRVFSFASR 791  
 DB 730 SLMEEGTPRDRQAQKDIPIILRPSLSHSETWIPEKXNGGDKKCEANLRVFSFASR 786  
 QY 792 ALRLTAPASLSVELSLNLEBAYVODLHPPGLSTRKVMKPKHQIPIVSGEELREB 851  
 DB 797 PLRLMSASLAVEMWLSNGEDAYVWRDLDFPRGLSPRKVMLOPHSRMPVSCHELEEG 846  
 QY 852 SRLSRALSNCVSPSIFRAGHGVVALQMMFNTLVNSMGDSVELHANYTCNNEDSDLEDN 911  
 DB 847 SLLTKTKLCNVSSSIFRAGHGVVALQMMFNTLVNSMGDSVELHANYTCNNEDSDLEDN 906  
 QY 912 SATIIIPILYPIINILIDQEDSTLYVSTPKGPKLHVYKMYQVRIOPSIDHNIPITLEA 971  
 DB 907 SAATHIPVLYPVNLTKEGENTLTVSTPKGPKQVQVHYQVRIOPSIDHNIPITLEA 966  
 QY 972 VVGVQVPSSEPTIQMSVQNEPPVPCYEDLER-LPDAEPLFGALFRCPVFRQIL 1030  
 DB 967 LVGVPRPSEDLITVWSVOTDPLVTCHESEDLPKPSSEAEQCPLEGVQFRCPVFRQIL 1026  
 QY 1031 VOVIGTLGVGEIEKSMPSICSSISISFNSSKHFLYGSNLSLAOVYKMDVYVEKML 1090  
 DB 1027 IGVTVTVELSKETKASTSTLSSISVSPSSKHFLYGSNLSLAOVYKMDVYVEKML 1086  
 QY 1091 YLYVLSGIGLLILIFIVLYKVGFFPKRLKEKMEKAGVYNGIPAEDEOLA-SCOE 1149  
 DB 1087 HVTYVLSGIGVLLIFILALYKVGFFPKRLKEKMEKAGVYNGIPAEDEOLA-SCOE 1146  
 QY 1150 GDPGLKLP 1157  
 DB 1147 KDMGCLER 1154  
 RESULT 3  
 RHWUB  
 cell surface glycoprotein CD11b precursor [validated] - human  
 N:Alternate names: complement receptor type 3 alpha chain; leukocyte adhesion protein Ma  
 leukocyte integrin alpha chain; neutrophil adherence receptor alphaM chain  
 C:Species: Homo sapiens (man)  
 C:Dates: 31-Dec-1992 #sequence\_revision 31-Dec-1992 #text\_change 09-Jul-2004  
 C:Accession: A31108; A28915; A41600; A20892; A32218; A46526; A26091; 152567  
 R:Corbi, A.L.; Kishimoto, T.K.; Miller, L.J.; Springer, T.A.  
 J. Biol. Chem. 263, 12403-12411, 1988  
 A>Title: The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, CD  
 B.  
 A:Reference number: A31108; MUID:88315033; PMID:2457584  
 A:Accession: A31108  
 A:Molecule type: mRNA  
 A:Residues: 1-1153 <COR>  
 A:Cross-references: UNIPROT:P11215; GB:J03925; NID:9187284; PTDN:AAA59544.1; PID:9307148  
 A>Note: part of this sequence was confirmed by protein sequencing  
 R:Arnaout, M.A.; Gupta, S.K.; Pierce, M.W.; Tenen, D.G.  
 J. Cell Biol. 106, 2153-2158, 1988  
 A>Title: Amino acid sequence of the alpha subunit of human leukocyte adhesion receptor M  
 A:Reference number: A28915; MUID:88257215; PMID:2454931  
 A:Accession: A28915  
 A:Molecule type: mRNA  
 A:Residues: 1-499,501-965, 'P', 967-1153 <ARN>  
 A:Cross-references: GB:M18044; GB:J03270; GB:M19664; GB:X07421; NID:9186935; PTDN:AAA594  
 A>Note: the authors translated the codon TAC for residue 1129 as Thr  
 R:Shelley, C.S.; Arnaout, M.A.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 10525-10529, 1988  
 A>Title: The promoter of the CD11b gene directs myeloid-specific and developmentally reg

A:Reference number: A41600; MUID:92073318; PMID:1663702  
 A:Accession: A41600  
 A:Molecule type: DNA  
 A:Residues: 1-9 <GB>  
 A:Cross-references: GB:M76724; NID:9180018; PTDN:AAA58410.1; PID:9553215  
 R:Arnaout, M.A.; Remold-O'Donnell, E.; Pierce, M.W.; Harris, P.; Tenen, D.G.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 2776-2780, 1988  
 A>Title: Molecular cloning of the alpha-subunit of human and guinea pig leukocyte adhesion  
 A:Reference number: A94193; MUID:88190151; PMID:2833753  
 A:Accession: A30892  
 A:Molecule type: mRNA  
 A:Residues: 917-1042 <AR2>  
 A:Cross-references: GB:M18044  
 R:Hickstein, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J.  
 Proc. Natl. Acad. Sci. U.S.A. 86, 257-261, 1989  
 A>Title: cDNA sequence for the alphaM subunit of the human neutrophil adherence receptor  
 A:Reference number: A32218; MUID:89098893; PMID:2563162  
 A:Accession: A32218  
 A:Molecule type: mRNA  
 A:Residues: 9-1153 <HIC>  
 A:Cross-references: GB:U04145; NID:9189068; PTDN:AAA59903.1; PID:9386975  
 A>Note: part of this sequence was confirmed by protein sequencing  
 R:Fleming, J.C.; Pahl, H.L.; Gonzalez, D.A.; Smith, T.F.; Tenen, D.G.  
 J. Immunol. 150, 480-490, 1993  
 A>Title: Structural analysis of the CD11b gene and phylogenetic analysis of the alpha-in  
 n during evolution.  
 A:Reference number: A46526; MUID:93123748; PMID:8419480  
 A:Accession: A46526  
 A:Status: not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-499,501-1153 <FLB>  
 A:Cross-references: GB:S52227; NID:9263047; PTDN:AA24821.1; PID:9263049  
 A>Note: the last three bases of intron 13, CAG, are included in some but not all mature  
 A>Note: sequence extracted from NCBI backbone (NCBI:P:121963)  
 R:Pierce, M.W.; Remold-O'Donnell, E.; Todd III, R.F.; Arnaout, M.A.  
 Biochim. Biophys. Acta 874, 368-371, 1986  
 A>Title: N-terminal sequence of human leukocyte glycoprotein Mol: conservation across sp  
 A:Reference number: A90664; MUID:87076671; PMID:3539202  
 A:Accession: A26091  
 A:Molecule type: protein  
 A:Residues: 17-31 <PIE>  
 A:Experimental source: granulocytes  
 R:Pahl, H.L.; Rosmarin, A.G.; Tenen, D.G.  
 Blood 79, 865-870, 1992  
 A>Title: Characterization of the myeloid-specific CD11b promoter.  
 A:Reference number: 152567; MUID:92144986; PMID:1346576  
 A:Accession: 152567  
 A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-9 <RES>  
 A:Cross-references: GB:M84477; NID:9180184; PTDN:AAA51960.1; PID:9553219  
 C:Comment: A common beta chain (CD18) forms a heterodimer with this chain to form Mac-1  
 C:Genetics:  
 A:Gene: GDB:ITGAM; CR3A  
 A:Cross-references: GDB:120599; OMIM:120980  
 A:Map position: 16p11.2-16p11.2  
 A>Note: promoter contains a GATA motif and two Sp1 consensus binding sites  
 C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homo  
 C:Keywords: alternative splicing; calcium; cell adhesion; glycoprotein; heterodimer; mag  
 P:11-16/Domain: signal sequence #status predicted <SIG>  
 P:17-1153/Product: cell surface glycoprotein CD11b #status experimental <MAT>  
 P:117-1108/Domain: extracellular #status predicted <EXT>  
 P:148-318/Domain: von Willebrand factor type A repeat homology <VWA2>  
 P:465-473/Region: calcium/magnesium binding #status predicted  
 P:530-538/Region: calcium/magnesium binding #status predicted  
 P:593-601/Region: calcium/magnesium binding #status predicted  
 P:1109-1134/Domain: transmembrane #status predicted <TM>  
 P:1115-1153/Domain: intracellular #status predicted <INT>  
 F:86,240,391,469,693,697,735,802,881,901,912,941,947,979,994,1022,1045,1051,1076/Binding  
 Query March 25.6%; Score 1563; DB 1; Length 1153;  
 Best local similarity 34.3%; Pred. No. 1,9e-99;  
 Matches 410; Conservative 210; Mismatches 464; Indels 110; Gaps 38;

```

QY 6 ITWAMALLSGFFFPAPASSYNLDVRCARSPSPRAGHFGYRLQV-GNGVIVAGAPE- 63
D 6 LLLALTLTCHGF-----NLDTEANMTFO--ENMAGFQSGVVOLOGSRVNVGAPGEI 54
QY 64 --GNSGTSLYCCSGTGCHLPVTLR-GSNYTSKYLGMTLATPDIDGSLIACDPGLSRTCD 120
D 55 VAAHQRGSLYCCDSTGSCBPIRLQVPVEAVNMSIGLSIAATSPPLIACGPTVHQCS 114
QY 121 ONTYLSGLCYLFRONLOGPMLQGRPGQECIKG----NVDLVPLFGDSMSLQDPBFOKITL 176
D 115 ENITVKGCLCFPGSNLR-----QOPKQPEBALRGCPQESDIAFLIDSGSGLIIPDFRPMK 170
QY 177 DEMKDVKMLSNSTSYOFAVVOFSTSYKTEPDPSPDYVKRDPDALIKYKMHMLLTNTFGA 236
D 171 EFVSTVMEQLKKSNTLPSLMQYSEEFRIHFHFKEKQNNPNRSLVKEPTQLGLGTHHTATG 230
QY 237 INYVATEYFEBELGARPATVYLLIITDGE--ATDSGNIDAKD-----IRYIIGIKH 289
D 231 IRKYVRELFNITNGARKNAFKILVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVDA 290
QY 290 FOTKESOBTLHKFAPSKAPSEFVKLIDTFEKLKDLFTBLQKKIYVHGSKQDLSFNNEL 349
D 291 FRSEKSRQELMTLASKPRPDHVPQVNNPEALKTIONLREKIFALBEGYTSSSPFEHEM 350
QY 350 SSSGISADLSRGHVVAVGAKDWAGFPLDKADLQDPTFGNEPLTPEVRAGYLGYYVT 409
D 351 SOEGFSAITNGPLSTVGSYDNAVGVF-LYTSKEKSTFINMTRVDSMDADATLGVAAY 409
QY 410 WLPBQKTSLLASGAPRYQHMGRVLLFOBPQGGHWSVOITHTQIGSYGGBELGCVYD 469
D 410 -IIRNRVQSLVTLGAPRYQHTGLVAMFR--ONTGMENANAVKQIGLAVYGASLCSYDV 466
QY 470 DQDETELLILGAPLFYGEORGGRVFIY-----ORQUGFEVSHLOSDPYPLGRGEA 524
D 467 DSNSTDLVTLGAPRYHQIRGQVSVCPRLRGGQAPKQCAV--LYBQOQPMGRFAA 524
QY 525 ITALTIDINGDLVAVAGAPLEE--QGAVYIFNGRHG-GLSPQSORIEGTQVLSGIQWF 581
D 525 LTVAGDVAGDGLTVATGAPBEDNRGAVYFHTGSSGSIKPSHSQIRASGKSLPRLOYF 584
QY 582 GRSHGVKDELEGGDLAVVAGAESOMITVLSRPVVDVMTLMSFSPDAEIPVHEVECSYTS 641
D 585 GQISGGGDLTMDGIVDLTVGAOGHVLLRQOPVLRVAKIMEFPRBEVAVRVFECNOQV 644
QY 642 NKMEGVNITICFOI-KSLYPOF-QGRVAMLTVTLQDGHRTRRGLFPGGRHRLRNI 699
D 645 -KGEKAGRVYCLHVKSTRRLRLEGQIQSVVITDLDLDSGRPHSRVAFNETKNSKTRQT 703
QY 700 AVT-TSMSCDTPSFHFVPCVODLISPIVNSINFSLMBEETPRDQAGKDIPIILRPSL 758
D 704 QVLGLTQCETLKLQLPNCIEDPVSPYLRNLFSL--VGRPLS--ANGN-----LRVYL 753
QY 759 HSEFWEL-----PREKNGEDKCKEANLRVSPSPARSALRLTAPASISVELSLSNLEED 813
D 754 AEDQKRFETALPPEKKNCGNDNIQDDLSITFSFMSLDCLVVGGRBENVTVTRANGED 813
QY 814 AYWQDLHFPFGSPFRKVENL---KPHSQIPVSCBELPERSRLRL---SCNVSSPI 867
D 814 SYRQVTFPFFPLDLSYRKVSTLQONORSWRILCES--ASTBVSGLAKSTCSINMPI 871
QY 868 FKAGHVALQWFFNTLVNSWGDSEBELTANTYCNNEBDLLEDSATTI---IFLVPIN 924
D 872 FPEKSEVTFNTFPVDSKASLGKLLKANTSEN---MPTNKTEFOLELVKAVY 927
QY 925 ILIDQDEBDSLTVSFTEPKGIHOVKMYQVRIQPSIHNDNIPTLEAVVGPQPSBGP 984
D 928 MYVTSHGVTKYLNTFASENTSRYWQHQQYV---SNIGQSRIP-LSLVLVPLVRLNQVI 983
QY 985 THQNSVQMEPPV--PCHYEDLERLPDAEPCLGALFRCPVY-----1024
D 984 WDRPOVTSSENLSTCHTK--ERLPSHD--FLAEKRAVPVNCISIAVCORIQCDIPFG 1039

```

```

QY 1025 PROEILVQVITGLTELYGEIAS-SMPSLCSLSISFNSKHFLYGSNASL-AQVWAKVD 1082
D 1040 IQEERFNATLKNISPDWYITSHNHLIVSTABILFNDVSFTLLIPGGAVRSQTERKVE 1099
QY 1083 VYERKQMLYLYVLSGIGLLILLIPLVLYKVGFPFRNLKKEKBAGRGVNGIIP 1136
D 1100 PFEVNPPLPIVSSVSGILLALLITATLYKLGFFKRYQKDYMMSEG-GPGABP 1152

RESULT 4
RWHUC
cell surface glycoprotein CD11c precursor - human
N/Alternate names: leukocyte adhesion receptor p150,95 alpha chain
C/Species: Homo sapiens (man)
C/Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text_change 09-Jul-2004
C/Accession: A36584; A35543; S00864
R/Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A.
J. Biol. Chem. 265, 12750-12751, 1990
A/Reference number: A36584
A/Contents: extratum
A/Accession: A36584
A/Molecule type: DNA
A/Residues: 1-1163 <COR>
A/Cross-references: UNIPROT:P20702
A/Note: this revision to the sequence from reference A35543 includes the carboxyl end
R/Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A.
J. Biol. Chem. 265, 2782-2788, 1990
A/Title: Genomic structure of an integrin alpha subunit, the leukocyte p150,95 molecule.
A/Reference number: A35543; MUID:90153906; PMID:2303426
A/Accession: A35543
A/Molecule type: DNA
A/Residues: 1-834 <CO2>
A/Note: this sequence has been revised in reference A36584
R/Corbi, A.L.; Miller, L.J.; O'Connor, K.; Larson, R.S.; Springer, T.A.
EMBO J. 6, 4023-4028, 1987
A/Title: cDNA cloning and complete primary structure of the alpha subunit of a leukocyte
A/Reference number: S00864; MUID:8816645; PMID:3327687
A/Accession: S00864
A/Molecule type: mRNA
A/Residues: 1-755, 'U', 757-1163 <CO3>
A/Cross-references: GB:W81695; EMBL:V00093; NID:g487829; PIDN:AA5180.1; PID:g487830
A/Note: part of this sequence was confirmed by protein sequencing
C/Comment: A common beta chain (CD18) forms a heterodimer with CD11b to form Mac-1 on mye
C/Genetics:
A/Gene: GDB:ITGAX; CD11C
A/Cross-references: GDB:119758; OMIM:151510
A/Map position: 16p11.2-16p11.2
C/Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homo
C/Keywords: calcium; cell adhesion; glycoprotein; heterodimer; magnesium; tandem repeat;
F/1-19/Domain: signal sequence #status predicted <SIG>
F/20-1163/Product: cell surface glycoprotein CD11c #status predicted <MAT>
F/19-319/Domain: extracellular #status predicted <EXT>
F/1108-1133/Domain: transmembrane #status predicted <TM>
F/1134-1163/Domain: intracellular #status predicted <INT>
F/61,89,392,697,735,899,939,1050/Binding site: carbohydrate (Asn) (covalent) #status pre

Query Match 25.0%; Score 1526.5; DB 1; Length 1163;
Best Local Similarity 35.0%; Pred. No. 6:5e-97;
Matches 421; Conservative 193; Mismatches 473; Indels 115; Gaps 40;

QY 12 ALISGFFFPAPASSYNLDVRCARSPSPRAGHFGYRLQVNGNG-VIVAGPE---GNSI 67
D 6 LALLLFTALATISGFNIDTEELTAFRVDSAG--FGSSVQVYANSWVNVGAPKQITANQT 63
QY 68 GSLYCCSGTGCHLPVTLR-GSNYTSKYLGMTLATPDIDGSLIACDPGLSRTCDQNTYLS 126
D 64 GGLYCCSGTSGACBPIGLQVPRPAVNMISGLSLASTTSPQLLACGPTVHNEGGRMYLT 123
QY 127 GLCTLPKQNLQGR-MIQGRP-GFQECIKGNVULVPLFGSMSLQDPDEPKLIDPMKDV 163
D 124 GLCTFL-----GPTQLQRLPVSRQCPROBODIVFLIDSGSISRRNFATMMNFVRAVI 178

```

```

QY 184 KKLSTSYQFAAVQSTSYKTEPFSDYVKRQDPALHGVKMLLTNTFGAINVATR 243
DB 179 SQRQPSQFSLMOSNKFQHTFTEBERFRTSNPLSLASVQLOGFTTATRIQNVHR 238
QY 244 VREBELGARPDATKVLIIITD---GEATDSGNI---DAAKDIIIRYIIGIKHFOYKES 295
DB 229 LFNASVGARDAATKILIVITDGKSGDSDYKDVIPMDAA-GIIRYAIQVGLARQNNNS 297
QY 236 QETLAKFKASKPASEPVKILDTFEKLDLFTLEOKKIYVIEGSKODLSFNNELSSGIS 355
DB 239 WKELINDASKPSEOHENIFKVEDPADIOMOLKEKIFALIEGTETSSSEFELEMAGEPS 357
QY 356 ARLSRGHAVVGAAGKADWAGFLDKADLDQDTPIGNBELTBEVAGVYVTVLPSRQ 415
DB 358 AVFTPDGAVLGAAGVSTMSGAP-LYPPNMSPTFIMNSQENVMDSDYGIS-TELALWK 415
QY 416 KTSLSASGAPRYQHMGRVLLFOBPQGGHMSQVOTIHGQISYSGELGCVNDVODGET 475
DB 416 QVQSLVLGAPRYQHNGKAVIF--TVYSRQMRKABVTGQISYSGASLCSVDVTDGST 473
QY 476 ELLILGAPLFYGEORGRVFIYOR---ROLGFEBSVBLQDGPYPLGFGAATLTDI 531
DB 474 DVLVLGAPHYEQTGGQVSVCPPLPRGMRRWMCDAV--LYGEGHPWGRFGAALTVLGDV 531
QY 532 NQDGLVDAVGAPLBEQ--GAVYIRNGRH-GLSQPSQRIQTQVLSGIOMFGRSIHCV 588
DB 532 NQDKLTDVIGAPGEENRGAVYLFHGVLPSPISHSQRILAGSOLSSLTQFEGALSGG 591
QY 589 KDLGEGDLADVAGASQMIIVLSRPPVDMVTLMSFSPAEIVHVEGCSYTSNKKKGV 648
DB 592 QDLTODGLVDLAVGARGQVLLRTRPVLMVGVSMQFIPRHSAPBECEQVYSS-QILY 650
QY 649 NITTFQIKSLYPOFQGR--LVANITTYTLQDLGHRTRRRGPPGRH-ELRNNIAVTSW 705
DB 651 QSNICLYIDIKRSKNLLGSRDLQSVTLDALDPGRLSPRATQERTNNLSRVRLGKA 710
QY 706 SCTDSSFNHPVVCYODLISPIVNSLNFSLMEBEGTRDQAQKDIPT--LAPSLHSR-- 761
DB 711 HCBENRLLLPSCVEBSVPTITRLNFTL-----VGPPLAFRNLPMLAADAQ 758
QY 762 ---TWBIPEKKGCEGKCEANLRVSPARSALRLTAPASLSVLSLNEEDAVWVQ 818
DB 759 RFTTSLPPEKNGCADHICQDNLGISFSFPGKSLIVGSLNLEBVMWMDNGEDSYGTT 818
QY 819 LDHAPPPGLSPFRKVEMLKPHSQ---IPVCEELPEBSRLSPALSCNVSSPIFKAGHSA 875
DB 819 ITFSHPAGLSYRYVAEGQKQGLRLSLHLTCDAPVGSQ-GTWSTGRINHLIFRGAQIT 877
QY 876 LQMMFNTLVNNSWGSVELHANVTCNNEDSDLEDNSATTI--IPILYPINILIQDQD 932
DB 878 FLATPDVSPKAVLGRLLLTAVNSEN---TPRTSKTTPOLELPVKYAVTVVSSHQ 933
QY 933 SFLVVSFTRPKPK-LHQVKNVQVRIQPSIHQHNIP-----LEAVGV 975
DB 934 FTKYLNFSSEKESKSVANHRQVN---NLGQRDLPVSLNFWVPELQEAVMQVESH 990
QY 976 POPPEGPIITHOMSVQMEPPVCHVEDLERLPDAAPCPLGAL-TRCPV---VPROELIV 1031
DB 991 PQNPS---LRCSSEKIAFPASDPLAHIQKN-VLDGSIAGCLRRCVDPSPVSEBELD 1045
QY 1032 QVITGLTEL--VEIEASMSFSLCSSLISLFSNKKFHLGYNASLAQVVMKVYVEKOM 1089
DB 1046 TFKGNLSFGWVROI-LQKVSIVSVVALETFTDSVVSOLPGOEAFMR---AQCTTVLEKK 1101
QY 1090 LY---LVYLSGIGGLLILLLFIYLYKYGFPRKMLKEKMEAGRG---VPNG--IPADS 1140
DB 1102 VAMPPLVIVGSSIGLLALITAVLYKVGFKQYKEMMERANQAIAPENGTOTPSPPS 1161
QY 1141 EQ 1142
DB 1162 EK 1163

```

```

RESULT 5
S00551
leukocyte surface glycoprotein Mac-1 alpha chain precursor - mouse
NAlternate names: complement-3 receptor alpha chain
CSpecies: Mus musculus (house mouse)
CDate: 30-Sep-1989 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
CAccession: S00551; 159078
R.Pirela, R.
EMBO J. 7, 1371-1378, 1988
A>Title: Amino acid sequence of the murine Mac-1 alpha chain reveals homology with the
A.Reference number: S00551; MUID:88312584; PMID:3044779
A.Accession: S00551
A.Molecule type: DNA
A.Residues: 1-1153 <PT>
A.Cross-references: UNIPROT:P05555; EMBL:X06440; NID:g52982; PID:CA30479.1; PID:g52983
A.Note: the authors translated the codon CAC for residue 569 as Gln
R.Sastre, L.; Roman, J.M.; Teplow, D.B.; Dreyer, W.J.; Gee, C.E.; Larson, R.S.; Roberts,
Proc. Natl. Acad. Sci. U.S.A. 83, 5644-5648, 1986
A>Title: A partial genomic DNA clone for the alpha subunit of the mouse complement recep
A.Reference number: 159078; MUID:86287312; PMID:2942940
A.Accession: 159078
A.Status: Preliminary; translated from GB/EMBL/DBJ
A.Molecule type: DNA
A.Residues: 11-44 <RES>
A.Cross-references: GB:M14293; NID:g198993; PID:AAA39484.1; PID:g554193
C.Genetics:
A.Gene: Mac-1
C.Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homo
C.Keywords: cell adhesion; glycoprotein; transmembrane protein
F.11-16/Domain: signal sequence #status predicted <SIG>
F.117-1153/Product: leukocyte surface glycoprotein Mac-1 alpha chain #status experimental
F.1148-318/Domain: von Willebrand factor type A repeat homology <VWA>
F.1106-1129/Domain: transmembrane #status predicted <TM>

Query Match 24.8%; Score 1514.5; DB 2; Length 1153;
Beet Local Similarity 33.8%; Pred. No. 4.3e-96;
Matches 407; Conservative 188; Mismatches 481; Indels 129; Gaps 36;

QY 6 ITWAMALLSGFFFAAPASSYNDLVRGARSPSPRAGHFGYRLVQ-GNGVIVGAPREG 64
DB 6 LLVVALMLCHSF-----NLDTHEHMTQENAKG--FGQNVVQGGTSVVVAAPGEA 54
QY 65 ---NSTGSLYCCQSGTGCHLPYTR-GSNYSKTLQMTLATDPDGSILACDPLSRTCD 120
DB 55 KAVVQTGALXQCDSTSCHPRLQVPPREAVNMSLGSLAVSTPQQLACGPPVHQCK 114
QY 121 QNTYLSGICYLFRNLQGMLOGRPGQECIKGAVVDLVLPDGSMSLOPBEFQKILPFMK 180
DB 115 ENTVVNGCYLFGSNLRLPPQQPPEALRECPQSSDIVLFDGSGSTINIIDFQMKEFVS 174
QY 181 DVMKLSTSYQFAAVQSTSYKTEPFSDYVKRQDPALHGVKMLLTNTFGAINV 240
DB 175 TVMQQFKSKSLFELMQYSDFRILHFTNDPKRPSRSNHSPIKQDNGRKTKASGRKV 234
QY 241 ATEVREBELGARPDATKVLIIITDGE---ATDSGNIADAQ---IIRYIIGIKHFOYK 293
DB 235 VRELFTHTKNGRENAAKILIVITDGEKFGDPLDYKDVIPMDRAAGVIRYVGVGNAEFKP 294
QY 294 ESQSTLHKFKASKPASEPVKILDTFEKLDLFTLEOKKIYVIEGSKODLSFNNELSSG 353
DB 295 QSRBELDTIASKPGENHFOVDNFEALNTIONQKEKIFALIEGTQSTGSFHEMSQEG 354
QY 354 ISADLSRGHAVVGAAGKADWAG-FLDKADLDQDTPIGNBELTBEVAGVYVTVLPSR 412
DB 355 FSASITSGPLGSGVSDMAGAFIVTSKD-KVTFINTTRVDSMDMDATVAGASAVI- 411
QY 413 SRQTSLSASGAPRYQHMGRVLLFOBPQGGHMSQVOTIHGQISYSGELGCVNDVOD 472
DB 412 LRNVQSLVIGAPRYQHNGKAVIF--NFTWTPHNTSIKSQISYSGASLCSVDMDAD 469
QY 473 GETELLILGAPLFYGEORGRVFI--YOROLGFEBSVBLQDGPYPLGFGAATLTD 530
DB 470 GNTMLILGAPHYEYKTRGGQVSVCPPLPRGARQCEALHGDGHPWGRFGAALTVLGD 529

```





Db 1022 STDHLKRTIIDCNTCKPATTCNL- : TSSDISQVNSVLLMKPTFKISYFSSLNTITRG 1079

QY 1062 SKHFLLYSNASIA-----QVAKVDVVEKQMLYLYVSGILGILLIFVL 1111

Db 1080 ----ELREBNASLVSSNQKRELAIQISDGLPERVFLVYLLISAPAGILLMLLIAL 1135

QY 1112 YKVGFFKRNLEKME 1126

Db 1136 WKIGFFKRLPKKME 1150

RESULT 7

A35854

Integrin alpha-1 chain precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 23-Oct-1990 #sequence\_revision 13-Sep-1991 #text\_change 09-Jul-2004

C:Accession: A35854; S11243

R:Gnathus, M.; Large, T.H.; Houde, M.; Tawil, J.W.; Barton, A.; Each, F.; Carbonetto, J. Cell Biol. 111, 709-720, 1990

A:Title: Molecular cloning of the rat integrin alpha-1-subunit: a receptor for laminin A

A:Reference number: A35854; MUID:90338125; PMID:2380249

A:Accession: A35854

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-1180 <INP>

A:Cross-references: UNIPROT:P18614; GB:X52140; NID:956493; PIDN:CAA36384.1; PID:956494

C:Keywords: cell adhesion; cytoskeleton; transmembrane protein

P:1170-345/Domain: von Willebrand factor type A repeat homology <VMA2>

Query Match 18.2%; Score 1112.5; DB 2; Length 1180;

Best Local Similarity 27.9%; Pred. No.2.9e-68;

Matches 351; Conservative 221; Mismatches 457; Indels 231; Gaps 52;

QY 4 SCITVAMALISGFFFAASSYNDVFGARSPFPRAGRHFGIRVLQV---GNGVIYV 59

Db 14 ACIMVLITVIL-GF-----CVSFNDVAKNSMSFSGP-VEDMFGYVQOYENEBEKWYLIG 65

QY 60 APDEGN---STGSLYQCGSGTGCLP-----VTLRGSNTSKYLGMTLATD 102

Db 66 SPLVQCPARPGVDYKCVGRBRAPCVKLDLPVNTSLPNTVEIKENNT--PSTLVTN 122

QY 103 PTDGSIACDPGLSRTCDONTYLSGLCYLFRONTLOGPMLQGRPGFQECIKGNVDLFLFD 162

Db 123 P-NGGFLLACGPLVYARCGHLHTTGICSDVPTPQ--VVNSFAPVQEC-STQGLDIVLVD 178

QY 163 GMSGLQDPBEFOKILDFMDQVKK--LSNTSYQFPAVQFSYKTEPDESDYVKKRDPAL 220

Db 179 GSNSTYF--WESVIAFLNDLTKRMDIGPKQVQVIGYGENVTHBFNLNKY----- 227

QY 221 LKHVGMILLNTRG-----AINVATVEYFRELGRARDATVLLITDGEATD 269

Db 228 -SYTEEVVAANKIGRGGLQTMALGIDTRKKAFLFARARARGVKKQWVIYVDGSHD 286

QY 270 SGNIDAA-----KDLIRYIIGIGKHF-----QTKESQETLHKASKPRASE-FKILIDTF 317

Db 287 NYRLKQVYQDCEDENIQFSAIILGHVYKGLSTBKPEYBEIKSLASBETGHHFNVDEL 346

QY 318 EKLKDLFTLQKLIIVIEGTSKODITSPFMELSSSGISADLSRGAHVAVGAVGADWAGGF 377

Db 347 -ALVTIVKALGERIPALBATDOSAPSPMEMSGQGFSAHYSQDMVLLGAVGADVMNGTV 405

QY 378 LDKYKD-----LQDDFTIGNEPLTPBYRAGLGYTV--TWLPSQKTSLLASGAPR 426

Db 406 VMQKRNQVVIPIHNTTFQTEPAKMEPL-----ASTLGATVNSATIPG---DVLIAQPR 457

QY 427 YQHKGRVLLFOEPQGGHMSQVOTIHGTQIGSYFEGELCGVDVQDGETELLILIGALFY 486

Db 458 YNHGQGVYIYK--MEDGNINILQTLIGRQIGSYGSYVTTITDIDKDSYTDLLVGAQMVM 515

QY 487 G--EQRGRVFLYQRRQLGFEEVSEIQ-----GDPGYPLG-RFEGAIT 526

Db 516 GTEKEQCKVVYVAVNQRRFQWMSLEPIROTCCSLKDNCKTENKNEPFGAAGFGAIA 575

QY 527 ALTLINGDLVAVGAPLBEQ--GAVYINGRHGGLSPQSGRIESTQVLSGIQWFGRS 564  
Db 576 AVKQLANDGFDDVVIAGPLBEDDHAGAVYIYHGSGKTIKREAYARISGGGDKTKLKEFGOS 635  
QY 585 IHGVQDLEGDGLAVAAVGAESQMTVLSSRPVMDVTLMSFPAIPVHEVECSYSTSNKM 644  
Db 636 IHGEMDLNGDGLDVTYIGIGAGNALFWARDVAVVKTVMNEPKNWIKQKNC--RVBGE 653  
QY 645 KEGVNTITFCQIK-----SLYPQOGRVLAMITLYTLQDGHRTRRRGLPGRG-HELR 697  
Db 694 TVCINATICEFVKLKSKEDSIYE-----ADQYRTVTLDSLQISHSFSGTQERKIQ 746  
QY 698 NIATYMSCTDFEFHFPVCYODLISPINISLNPMSLMEEGSTRDQAGKDIPELIRPS 757  
Db 747 NIYVRES-ECIRHSFYV-LDKHPQDSVRVTLDFNLDPEN-----GVLVDDA 792  
QY 758 LHSETWE-IPEKKCGGRDKKCEANLRFVSFSPA-RSRRLRLTAFASSLVELSLNLEBDAY 815  
Db 793 LPNSVHEHIFPADCGNKKERCISDLTLNASTTEKSLIYVSGHDKFVSLTVKNKGSAY 852  
QY 816 WVQDLHPFPGGLSFRRKYMCLKPHSQDLPVSCBELPEBSRLSLRSLSCNVSSPIFKAGHVA 875  
Db 853 NTRVYVGHSPFLRISGIEBIQD-----SCES-----NQWITCVGVPIRAGETV 899  
QY 876 LQNM--FNTLVNMSGVSVELHANVTCNEDS--DLIEDNSATTIPLIYINI-LIODQ 931  
Db 900 FKILFOENT---SHLSENALIHLSATSDEEPLESLNDNEVNISIPKVEVGQFYSSAS 956  
QY 932 DSTLYVEFTPKPKCI-----HGVKMWQVRIOPSIHQNIPTLEAVVGVQPPSEG- 982  
Db 957 EKHISVANETIEPFINSTEDIGNEINVFYTIKRGHF--PMPEIQLSISFNLTRADGY 1013  
QY 983 PITQWQSVOMEPPVPCHYEDE-----RUPDAAPC----- 1013  
Db 1014 PVLPIGCMSSDNNVNCPRSLBDFPGINSKQMTISKBVLKRGTIQDCSGTGVATTIC 1073  
QY 1014 --LFGALPRCPV---VRQELIVQVIGTELV--GELEASMSLCSLSISFNSKHFH 1066  
Db 1074 SLPSDDLSQVNVSLMLKPFPIRAHFPSSLMLTLRGELKSEN-----SSLTSSNNRR- 1126  
QY 1067 LYGNSASLAQVVMKVDPVVEKQMLYLVLSGIGLLLLIFIVLYVGVGPKNLKEMK 1126  
Db 1127 -----ELAIQISK-DGLPGRVPLWTLVLSAPAGLLMLLILALMKIGFPKPKLKKHE 1179

RESULT 8  
145914  
Integrin alpha 2 subunit - bovine (fragment)  
C/Species: Bos primigenius taurus (cattle)  
C/Date: 16-Aug-1996 #sequence Revision 16-Aug-1996 #text\_change 09-Jul-2004  
C/Accession: 145914  
R/Kamata, T.; Puzon, W.; Takada, Y.  
J. Biol. Chem. 269, 9659-9663, 1994  
A>Title: Identification of putative ligand binding sites within the I-domain of integrin  
A/Reference number: A54402, MUID:94193647; PMID:7511552  
A/Accession: 145914  
A/Status: preliminary; translated from GB/EMBL/DDAU  
A/Molecule type: mRNA  
A/Residues: 1-1170 <AM>  
A/Cross-references: UNIPROT:P53710; GB:I25886; NID:g439695; PIDN:AAH59255.1; PID:g439696  
P161-336/Domain: von Willebrand factor type A repeat homology <VMA2>

Query Match 16.6%; Score 1012.5; DB 2; Length 1170;  
Best local similarity 28.2%; Pred. No. 2,4e-61;  
Matches 346; Conservative 209; Mismatches 459; Indels 211; Gaps 56;

QY 25 SYNDVAGARSPSPRAGRHFGRVLYQV---GNGYIVAGPBG---NSTGSLYQC--QS 75  
Db 18 AYNVGLPKAKTIFSGP--SSQPGYAVQDFINPKGMLLVGSPWGGFPRKRMGDVTKCPVDL 76  
QY 76 GTGHCLEPVTLRGNS-----YTSKYLGMTLATDPTDGSILACDPLSRCTCDONTYLSG 127

```

Db 77 STTCEKLNQSTSMNSVTEKTNMSLGLTLTRNVGTGFLTCGPMAOQCGSQTYYTG 136
Oy 128 LCYLFRONLQ-----GPMLOGRPGFQECIKGNVDLVPFLPDGSMSLQDEPFQKILDPMDV 182
Db 137 VCSVSPFOPLRTSPAPAVQTCPSF-----IDVVVCDSENSTYF-----MDAVNMF 183
Oy 183 MKK-----LSNTSYQFAAVQSTSYKTEPDFSDYVRKRDPAALKHVKNML-----LTN 232
Db 184 LEKFQGLDIDPTKQMLQIYANPRVFNLMNPF---KSDENMKANSQTFQYQGDLTN 240
Oy 233 TFGALNVAATEVREBELGAPDATVLLITDGEATDSGNIDAAD-----IIRYITGI 286
Db 241 TFKAIQYARDATYATPAAGRPATKVVVVVVDGSHSDSKAKAVDQCNDKNIIRFGIAY 300
Oy 287 -----GKHFOTKESQETLHKFASKRPS-BPFKILDTPEFKLDLTELQKTIYVIGTSKQ 340
Db 301 LGYLNRAADTKNLKEIKALIASLPTENHFRVSDADLEKACT-ISEQIFSLBGT-VQ 358
Oy 341 DLTSFNNELSSSGISADLSRGHAV--VGAAGAKDWAGFLDLKADLDPTFIGNEP--- 394
Db 359 GGDNFQWEMSGVGSFAEYSPQNNILMLGAVGAYDMSG-----TVVQKTPHGL 406
Oy 395 -----LTPEVAGIYLTYYTWLPSRQKTSILASGAPRYQMGKVLVLPQEQGGH 444
Db 407 IFSKQAFQIILQDRNHSYLGYSVASISTGNSVHFVA-GAPRANVTGQIYIVSVNE-NGN 464
Oy 445 MSQVOTIHTQIGSYFGELCGVDVDQDETLLIGAPLFYGE--QRGGRVFTY--QR 500
Db 465 VTVIQQSGDDIGSYFGSVLCANDVNKOTITDVLIVGAPMTNMDLKEBGRVLYFTITKG 524
Oy 501 QLGFEVSELOQDPGYPLGRFGEAITALTIDINGDLVDVAVGAPLEEQ--GAVYIFNGRH 558
Db 525 ILNMHQF--LEBPGNLEVARFGSALALSDINMDGFNDVIVGSPLENQSGAVYIYNGHE 582
Oy 559 GGLSPQSPQREBQ--VLSGIQMGKRSIHVKYLEBGLADVAVGASQMTIVLSRPV 616
Db 583 GMILRYSQKILGSRAPASHQYFGRSLDYGDLNGSITDVSVGAGVQVVOVMSOSIA 642
Oy 617 DMVTLMSFPAIPVHEVCSYSTSNKMEGVNITICFOISLVPQFGRLVAMLTYYLQ 676
Db 643 DVSVDASTTPKTI-----TLANKAE-IKLKCTCSAK-FRPTNOMNOVA-IVNYIT 690
Oy 677 LD-----GHTRRRGLFPGGRHE-LRNIAVTTSMSTCFSPHFVPCVDLISPINSLNF 731
Db 691 IDEQOFSRVRISRGIFKENNERCLQKTMIVQAOQCSYIIHIGE-PEDIIISPLMCMNI 749
Oy 732 SLMEBEGTPRQORAGKDIPIRLPSL--HSET--WEIPKRCGEGDKCBAN--LRVS 784
Db 750 SL-ENPGT-----NPALEAVSEYVVFISIPFKKOCGDGVCISDLVINVQ 793
Oy 785 FSPARSLRLTLAFAS--LSVELLSNLEDAVWVQDLHFRPGISFPKXVEMLKPHQIP 842
Db 794 QLPATQOQPFIVSONKRLTFSVOLKMKESAHYITEIVDSENLFFFSMSM-----P 846
Oy 843 VSCBELPEBSRLSRALSCNVSPIFKAGHSVALQMMEN-TLVSSWGDSEYELHANYTCN 901
Db 847 VDGFEVTCQIASQKSVTCNVGYPALKSKQCVTFINDFMLQNLQNGASISFPA---LS 903
Oy 902 NEEDDLLEDNATTIIPILYPINILQ-----DOEDTLVYSFPKPKGKHQV 949
Db 904 ESOBENMADNVNKLSTLYDAEIHITRSTININFEVSLDGNVSSVHSPFEDISPKF--- 960
Oy 950 KHMVQVRIQSIHIDNIPTEEA--VVGVPQ--PSPSGPITHQMSVQMBE--PVPCGYE--D 1002
Db 961 --ISIKYTTG--SVVSMASVYIHIPOYTKDKNPLMYLTGVHTTDAQDISCEALINP 1014
Oy 1003 LERLPDAEPCLPGLFR-----CPVVFRQEI-----VOVITGLLEL-----VGEIE 1044
Db 1015 LKIQGTSSSVFSEBNFHIKELNCRITASCSNIMQWLDLQVKGEYPLFNVSTRIMNGFA 1074
Oy 1045 ASSM--PSLCSLSISFNSSKGFHLYGSNADLAOVNKKVADVVERKQMLYLYLGG--IGG 1100
Db 1075 ASTQVQVLTAAAEIDTYNPQIYVIEBNTVTIPLTIMK--PHEKVEVPTVIVGSVIAG 1131

```

```

Oy 1101 LLLLLIFIVLYKVFERNLKEKM 1125
Db 1132 ILLHLLVALILMKLGFPRKY-ERM 1155

RESULT 9
A3398
N:Alternate names: CD49b; platelet glycoprotein GPIa; VLA-2/collagen receptor alpha-2
C:Species: Homo sapiens (man)
C:Date: 30-Mar-1990 #sequence_revision 18-Sep-1992 #text_change 09-Jul-2004
C:Accession: A3398; B56793; A53117
R:Takada, Y.; Hemler, M.E.
J:Cell Biol. 109, 397-407, 1989
A:Title: The primary structure of the VLA-2/collagen receptor alpha(2)-subunit (platelet
A:Reference number: A3398; MUID:89308879; PMID:2545729
A:Accession: A3398
A:Molecule type: mRNA
A:Residues: 1-1181 <TAK>
A:Note: the authors translated the codon GAT for residue 802 as Gln, GTC for residue 803
R:Catimel, B.; Parmentier, S.; Leung, L.L.; McGee, J.L.
Biochem. J. 279, 419-425, 1991
A:Title: Separation of important new platelet glycoproteins (GPIa, GPIC, GPIC*, GPIIa and
A:Reference number: A56793; MUID:92061944; PMID:1953640
A:Accession: B56793
A:Molecule type: protein
A:Residues: 30-43 <CAT>
A:Experimental source: platelet
R:Zutter, M.M.; Santoro, S.A.; Painter, A.S.; Tsung, Y.L.; Gafford, A.
J. Biol. Chem. 269, 463-469, 1994
A:Title: The human alpha-2 integrin gene promoter. Identification of positive and negative
A:Reference number: A53117; MUID:94103255; PMID:8276836
A:Accession: A53117
A:Molecule type: DNA
A:Residues: 1-16, 'V', 18-21 <ZUT>
A:Note: references: GB:L24121; NID:9400342; PIDN:AAA1619.2; PID:9458353
C:Genetics:
A:Gene: GDB:ITGA2; CD49B
A:Cross-references: GDB:128031; OMIM:192974
A:Map position: 5q11.1-5q11.2
C:Keywords: cell adhesion; glycoprotein; heterodimer; transmembrane protein
F:1-29/DNA: signal sequence #status predicted <SIG>
F:30-1133/DNA: extracellular #status predicted <EXT>
F:1134-1154/DNA: transmembrane #status predicted <TM>
F:1155-1181/DNA: intracellular #status predicted <CYT>
F:105,112,343,432,460,475,699,1057,1074,1081/Binding site: carbohydrate (Asn) (covalent)

Query Match 16.1%; Score 985; DB 2; Length 1181;
Best Local Similarity 27.6%; Pred. No. 1,9e-59;
Matches 349; Conservative 210; Mismatches 484; Indels 220; Gaps 54;

Oy 8 VMAALLSGFFFPAPASSYVLDVGRSFPAPGRHFGYVLYOV-----GNGYVGAPE 63
Db 14 LVVIALSQGLNCLLA--YVGLPEAKIFSGP--SSQFGIYAVQFINKKMLIVGSPWS 70
Oy 64 G---NSTGSLYQC--QSGTGHCLPVTLRGSN-----YTSKYLQMTLATDPTDGSILA 110
Db 71 GPFENRMDGVYKCPVDLSTACEKLNQSTISIPNTEKMTNMSLGLLTRNMGTGGLFT 130
Oy 111 CDRELSTCQNTYLSGLCYLFRONLQ-----GPMLOGRPGFQECIKGNVDLVPFLPDGSM 165
Db 131 CGPLMAOQCGNQYTYTGVCSIDSPDQLSASFPAQPCSL-----IDVVVCDSEN 183
Oy 166 SLOPDEFQKILDPMDKVMKK-----LSNTSYQFAAVQSTSYKTEPDFSDYVRKRDPA 219
Db 184 STYF-----WDVAKFLKFFVQGLDIPKTYGVLQIYANPRVFNLMNPF----- 229
Oy 220 LKHKVKMLL-----LNTFGALNVAATEVREBELGAPDATVLLITDGEAT 268

```

```

Db 230 --KTEEMIVATSTQSGDGLTNTFGALQVARKTAYASAGGRSRATKVMVVTGDSH 287
Qy 269 DSGNDAAKD-----IIRYIIGI-----GKHPKESQETLHKASRPASE-FKILDT 316
Db 288 DSGMKAVYDQCNHNDILFGLAVAGYLRNALDITKILKALASIPTEKRYFNVSDE 347
Qy 317 FEKLDLFTLOKTIYVEGTSKODLTSPNMLSSSGISADISRGHAY--VGAENAKOMA 374
Db 348 AALLKAGT-LGEOFSIEGT-VGGDNFQEMMSQVGSADISSQNDIMLAGAVAFGWS 405
Qy 375 G-----GFLDLKADLDODTFIGNEPITPEVRAGYLGTYTWLPSROKTSILASGAR 426
Db 406 GTIVGKTSHGHLIPKQAVD-----QLIDRNHSSYLGYSVAALSTGESHTFVA-GAPR 458
Qy 427 YOMKRVALLFOEPQGGHMSQVQTHGTQIGSYFGSELGVVDVDDGTELLILGAPLFY 486
Db 459 AMYTOIYLYSVNE-NENITVIQARHGOIGSYFSGVLCSDVVDKDTITDVLVGAPEWM 517
Qy 487 GE--ORGGRVFIYGRORLGFEEVSELODPPGYPLGRPGBATLALDINGDGLVDVAVAP 544
Db 518 SDUKKEBGRVYLTTKGILGHOFLGEPGEGIENTRFSALMALSDIMNDGENDIVGSP 577
Qy 545 LEBQ--GAVYLPNGHNGLSPOPSQIRBGTQ--VLSGIQWFGRSIHGVNLEGGDLADVA 600
Db 578 LENQSGAVYIYNHOGTIRTKYSQKILGSDGAPRSHIQLYFGRSLDGYDGLNGDSITDVS 637
Qy 601 VGASEQMTVLSRPVVDVMTLMSFSPALIPVHEVECSYSTSNKKEGVNITTCPOIKSLY 660
Db 638 IGAFQVQVQVLMQSIADVAIEASFPEPKI-----TLVKNQAQ--IILKLCFSAK-FR 686
Qy 661 PQFOGRVLANLYTTLQD-----GHTRRRGLFPGGRHE-LRNNIATVMSGTDSSHPF 715
Db 667 PKQNNQVA-IYNNITLDDGSSSVTSRGLFKENNERCLQNMVWVNAQSCPEHITIQ 745
Qy 716 VCVODLIPINVLNFSLMEEBGTPRDQRAQKDIPIRLPSL--HSET--WEIPEFKN 770
Db 746 E-PSUVVNSLDLRVIDSL-ENRGT-----SPALBAVSETAKYFSLPFKID 788
Qy 771 CGBKKCEAN--LRVSPSPARSRALRLTAFAS--LSVELSLNLEDAVWQDLHPPG 826
Db 789 CGHDLCTISDLVDVROQIPAAQOEPIVSNQKRLLTFSVTLKNKESAVNTGIVDFSEN 848
Qy 827 LSFRTVEMLKPHSQIPVSCBELPESRLLSRALSCNVSSTPIFKASHVALQMKR- TLVN 885
Db 849 LFPASF-----SLPVDGTEVTQVVAASQKSVACDVGPRALKRQOVTFTINFENQON 901
Qy 886 SSMGDSVELHANVTQNNEDSDLEDNASATTIPIILYPINI-----LIQDQEDS 933
Db 902 LQNKSLSFQALSEQEBEK--ADNLVNLKIPILYDAEHLTRSTNINFEISSDGNP 958
Qy 934 TLVYSPFKPKIKHQVKMYQVRIQPSIHDNIPITLEA--VWVGPQPPSE-GRITHQMSV 990
Db 959 SIYHSEFEDVGRKF-----IFSLKVTG--SVPSMAVTIIHIIQYKKNPLMYLGV 1009
Qy 991 QMEP--PVPK-----HYDELEKLPDAEPCRLFGALFRCPVVERQ 1027
Db 1010 QTDKAGDISCNADINPLKIGQTSVSSVSPKSENFRTKELNCRJASCSNVTCMLKDVHNG 1069
Qy 1028 ELVVOVIGTLBVLGEIEASSMF--SLCSSLISNSNKHPLYSNNAQLQVWKKVVV 1084
Db 1070 EYFVNV--TRIMNSTFASSTFTQVQLTAAAEININVEIYIENVTYTIPLMIKRP-- 1125
Qy 1085 YEKQMLYLYVLSG--IGGLLLLLLIYLYVKGPFKNMLKEMMEAGRGVPGVNGIPRADEQ 1142
Db 1126 -EKAEPVGVIGISIIAGILLALLVALIMKLGFPRKX-EKM-----TKNPDEIDETTE 1178
Qy 1143 LAG 1145
Db 1179 LSS 1181

```

RESULT 10  
AS3213

```

Integrin alpha-E chain - human
C.Species: Homo sapiens (man)
C.Date: 19-Oct-1995 #sequence_revision 31-Mar-2001 #text_change 09-Jul-2004
C.Accession: A53213
R.Shaw, S.K.; Ceppek, K.L.; Murphy, E.A.; Russell, G.J.; Brenner, M.B.; Parker, C.M.
J. Biol. Chem. 269, 6016-6025, 1994
A.Title: Molecular cloning of the human mucosal lymphocyte integrin alpha(E) subunit. Un
A.Reference number: A53213; MUID:94164962; PMID:8119947
A.Accession: A53213
A.Status: preliminary
A.Molecule type: mRNA
A.Releases: 1-1179 <SHA>
A.Cross-references: UNIPROT:P36570; GB:L25851; NID:g457244; PTD:g457245
C.Genetics:
A.Gene: ITGAE
A.Cross-references: GDB:330801
A.Map position: 17p13
C.Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homo
F.199-371/Domains: von Willebrand factor type A repeat homology <YMA3>

Query Match 16.0%; Score 976.5; DB 2; Length 1179;
Best local similarity 26.0%; Pred. No. 7.5e-59;
Matches 330; Conservative 214; Mismatches 454; Indels 273; Gaps 47;

Qy 6 ITWAMMLSGFFFAASSYNLDRGARSPPRAGRHPGTYRL-----QVNGVTVG 59
Db 8 LCISALLALAA-----NVDV--ARPWLTGKGAAPVLSLHQDPSTNQTWLLVT 56
Qy 60 ARGSGNSTSLYOCOSGNH--CLPV-----TLRGSNTSKYLGTLATDPDGSILACDP 113
Db 57 SPKRKRTGFLRHSLYODELCHPVEHVPKPK-----RRKGVTVARS-HHGVLICIQV 110
Qy 114 GLSFTCDQNTYLSGLCYLFRONTLOGPML--QGRDGF----- 147
Db 111 LVRRPHSLSSBLTGTC-----SLGPDLRPAQANFDELVLDPDARVDTGDCYSNKEG 165
Qy 148 -----QECIKANVDLVFLPDSMSLQRPBFQKIDFM 179
Db 166 GGEDVNTARQRALKEEBEEDKEEBEEDKEEAGTIAIILDSGSDIDPDPORADFI 225
Qy 180 KDVMKKSNTSYQ--FAVOPSTSYKTEPDSYVKKRDPALIKHYKGM--LTNTF 234
Db 226 SNNKRNTEKCFECNPLVQVGVYQTFBURLD--SQDVWASLARQNTIQVGSVTKTA 282
Qy 235 GAINVYAVEVEREELGARPATKYLIIITDG-----EATDSGNIDAAKDIIRYIIGIG 287
Db 283 SAMQHVLDSIFTSHGSRARRKSKVMVVLTDGIGFEDPLNTTVINSRQKQVEHFAIGVG 342
Qy 288 KHPQTKSQETLHKFASRPASBEFKYIIDLTEPKLQDTELOKTIYVEGTSKODLTSPNM 347
Db 343 EEFKSARTARELNLIADPDETHAFKVTNNYMALDGLLSKLRVNIISMEGTVDAL--HY 399
Qy 348 ELSSSGISAD-LSRGHNVGAVGAKDWAGGLDKADLDODTFIGNEPITPEVRA----- 401
Db 400 QLAQIGFSAQILDERQVLDGAVGFDMWGGLLYDTSSRKRF--NQTAAAADABAQY 458
Qy 402 GYLQYTWLPSROKTSLLA--SGAPRYOHNGRYLFOEPQGGHMSQVQTHGTQIGSY 459
Db 459 SYLDVYAAVL--HKTGSLSYVAGAPQYKHNAN--FELQKEGEBAFLPYLBEQWGSY 513
Qy 460 FGGELGVVDVDDGTELLIGARLFYGBORGGHVFYQ--RROLGEBEYSELOGDGYP 517
Db 514 FGSSELCPVDIDMDSTFLVLAAPFYVNHGEGVVYVRLSEDDGSFSLARILSGHGFT 573
Qy 518 LGRFGEALITLTDINGGIVDVAAGAPLEBEGA-----VYFNRRHGLSPQPSORI 569
Db 574 NARFGPMAAMGDSQKLTIDVALGAPLBEGADGASFGSVIYNNHMGDLSLSPORI 633
Qy 570 EGTQVLSGIQWFGRSIHGVNLEGGDLADVAVAGASQMTVLSRPVVDVMTLMSFPAEI 629
Db 634 RASTVAPQLQYFGMSMAGGFDISGDLADITVGLIGAVVFRSPPVRLKYSMAFTSAL 693
Qy 630 PVHEVECSYSTSNKKEGVNITTCPOIKSLYPOQ--GRVLANLYTTLQDLGHRTRRGLF 688

```

```

Db      694 P1-----GNGVNVNRLCFEISSVTTSBSSGREALNFTLVDVGKQRR--- 739
Qy      689 PGRHELRARNIAVTTSMCTD-----FSHFPPVCVDLIP1 725
Db      740 -----LCCSDVRSCLGCLREWSSGQCEDLLMPTEGCEECBCFENA 783
Qy      726 NVSLNFSLMEBEGTRPDORAQOKDIP1L-RPSLSFTWEIPEFKNGCEDKCEANLAVS 784
Db      784 SVKYSYQOTPEG-----QTDHPQILDRTEREPALFQLPYEKACNKLFCVLAELQTA 836
Qy      785 FSPARSRALRLTAFAISLSELSLNEEDAYVQDLHPFPGLSFRKVMKPKHSQIPVS 844
Db      837 -TVVSQOELVGLTEKELTNLNTSGSDSVYTSMALVPRYLQAKR--MQKPPSP-NIQ 892
Qy      845 CEE-LPEESRLSLRSLSCNVSPIFK---AGHSVALQMMFNTLVNNSMGDSVELHANTC 900
Db      893 CDDPQPVASVLI---MNCRIQHPVLKRSSAHVSVMQLEENAFPRN---TADITVYTN 945
Qy      901 NNEBSDLLSDNSATT---IIPILPILNLLQODESTLYVS-----FTPKGP 944
Db      946 SNERSLANETHHTLOFRGFAVL-----SKPSIMYNTQGLSHKKEFLPHVGE 996
Qy      945 KIHQVKEMYQVRIQPSIHDHNIPTLEAVVGPQPPSEGPITHQMSVQMPVPCHYEDLE 1004
Db      997 NLFGAEYQIQICVPTKRLGLQVAVKCLT---RTQASTVCTMSQER---ACAYSSVQ 1047
Qy      1005 RLPPAEECLPGALFRGVVROEI-----LVQVITGLBELVGEIEMSMFSLCSSLST 1057
Db      1048 HVEEHSHVSCVIAADKENVTAAELSMDSBELLDVTELQILG-----I 1093
Qy      1058 SFNSKHFHLY-GSNASIAQVVMKVYVERKOMLY---LVYLSIGIGLLLLPIFYLY 1112
Db      1094 SFNNS-----LYEGLNAEHNR--KITVYFLDKETHSLPIIILKSGVGLVILVILVF 1147
Qy      1113 KVGFPPKMLKE 1123
Db      1148 KCGFFKRYKQ 1158

```

## RESULT 11

```

S44142
VLA-2 protein homolog - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S44142
R:Edelman, J.M.; Chan, B.M.; Uniyal, S.; Onodera, H.; Wang, D.Z.; Damjanovich, L.; Latze
submitted to the EMBL Data Library, January 1994
A:Description: The mouse VLA-2 homologue supports collagen and laminin adhesion but not
A:Reference number: S44142
A:Accession: S44142
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1178 <EDE>
A:Cross-references: UNIPROT:Q62469; EMBL:Z29987; NID:q473098; PIDN:CAA82877.1; PID:q4730
F:169-344/Domain: von Willebrand factor type A repeat homolog <WA2>

```

Query March 15 7\*: Score 959; DB 2; Length 1178;

Best Local Similarity 27.5%; Pred. No. 1.2e-57;

Matches 334; Conservative 219; Mismatches 468; Indels 194; Gaps 54;

```

Qy      25 SYNLVDRGARSPSPRAGRHFGRVLAQY---GNGVIVGAPGEG---NSTGSLVQC--QS 75
Db      26 AYVNGLPRAKILFSGP-SSGQFGYSVQDLTNPGQMWLVGSRSGPFRKMDVYKCPVDL 84
Qy      76 GTGICLPVTLGNSN-----YTSKYLGMTLATDPTDGSILACDPGLSRTCDQNTYLSG 127
Db      85 PLTACEKRLNQNASISNVTEIKTMSGLTLTRNPGTGFLTGPLMAHQCGNQYATG 144
Qy      128 LCYLFROULQ-----GPMLOGRPGQECIKKANDLVFLFDGSMISIQDPFQK--ILDPMK 180
Db      145 ICSVSPDFQFLTFSGSPAVQACPSL-----VDVVVVCDESNSIYFWEAVKNPLVKEVT 197

```

```

Qy      181 --DVMKLNTSNTSYQFAAVQFSTSYKTEFSDYVKRD-PDALLKVKHMLLNTFGAI 237
Db      198 GLDIDPKKT-----QVALIQYANBRRIIFNLNDPTEKDMQQAISFTRQHGDLNTPRAI 253
Qy      238 NYATAEVFRBELGARPDATVYLLIITDGEATDSGNIDA-----KDIIRYIIGI----- 286
Db      254 EFADYAVASQTSGGFRPATYVMVWVVDTEGESHDSKLTQVLIQQCNDBELIFGLAVLGYLN 313
Qy      287 GKHFQTESQETLHKFKASKPASE-FVKILDTPELQDLFELQKIVIEGTQKODLTSP 345
Db      314 RNALDTNLIKELKALNASTPERYFENVADAEALLERAGT-LBQQLFSLIGT--VQGGDNF 371
Qy      346 NMEISSSGISADLSRGHAV--VGAVGAKDWAGFLDKAD-----LQDTEIGNEPLTREV 399
Db      372 QMEAAQVGFSAADYAPQNDILMLGAVGAFDSGLTVQSTSKPIVFRQAR--DQVLDNRN 429
Qy      400 PAGLYGTVTWLPSRQKTSLLAGAPRYQMGRAVLFQEPQGGHMSQVOTIHGTQIGSY 459
Db      430 HSPFLGYSAALISTEDVHFVA--GAPRANYTGQIVLYSVNKK--QGNVTVLIQSHRGDQIGSY 487
Qy      460 FGSELQGVDDQDQGEETELLIGAPLFYGE--QKGRFPIYQRRQLAGEEYSELQGDGPY 517
Db      488 FGSVLCSDVDVKDQITDVLVGAFTYMDLKKKEGKYLLFTTKGILNQHFLEGPREGTG 547
Qy      518 LGRFGEAITALTDINGDLVDVAVGAPLEEQ--GAVYIFNGRRGSLSPQSPORIEGTQ-- 573
Db      548 NARFGSAIALSDIMDMGFVDVIGSVENENSGAVIYVNGHGTIRTKSQILSNGA 607
Qy      574 VLSGIQMFGRSINGVKDLESDGLADVAVGAESQMTVLSRPVVDMTVLMSPSPAEIPVHE 633
Db      608 FRRLQPFGRSLDGYGDLNDSITDVSIGALQVITQLMSQSIDVAIEALFTPDKITLLN 667
Qy      634 VECSTYSNMKMGKGVNTTICQIKSLYPOFGSLVANT--TYTQLDQHR--RGLF-P 689
Db      668 KDAK-----ITKLCTPRAB-FRPAQONNOVALLENMTLDAGHSRSRVTSGVFR 716
Qy      690 GGRHELRARNIAVTTSMCTD--FSHFPPVCVDLISPINSLNFSLMEBEGTRPDORAQ 747
Db      717 NSERFLQKMNVVNEVQKSEHHSIQK---SDVNPDLDRVDSL-ENGCT----- 764
Qy      748 KDIPPIRLPSL--HSET--WEIPEKNGCEDKCEANLAVSFPASRLRLTAF--- 798
Db      765 -----SPALAEVSEVVKFISIPFYKECGSDGICISDLILDVQ--QLPAIQOSFVSN 815
Qy      799 --ASLSVELSLNLEEDAYVQDLHPPPLSPRKVMKPKHSQIPIVSCDELPEESRLLS 856
Db      816 QNKRLLTYSVILKNGKESAVYTVVLAESSENLFASFSM-----PVDGTEVCEVGSSQ 868
Qy      857 RALSQVNSPFIYFAGHSVALQMMFNTLVNNSMGDSVELHANTCNNEEDSLLE-DNSATT 915
Db      869 KSVYCDVGYALKSSEQVYFTTINPDRYLQNLQNOQA---INPQAFSSQSTTNKADNSVSL 925
Qy      916 TIPIYPIINI-----LIQDESTLYVSTPKPKIKHQVKMYQVRIQPSIHD 963
Db      926 TIPLLYDAEHLTRSTININFEISDENAPSVIKSYVEDIGPKF-----IFSLKVTAG--- 977
Qy      964 HNIPTLEAVY--GVPPQPSF-GPIITHQMSVQMP--PVCPHYE-DLERLPDAABPCPGA 1017
Db      978 -SAVSNALVTYTHIPQYTKERKNPLVLTGLOTQOAGDISTAELNPLKLPHTL---PSV 1032
Qy      1018 LFR-----CPVV-----PROELIVQYIGLRLVGEIEMSMF---S 1050
Db      1033 SFKKNENRHRKELDERTSSNITCMKLDLMAKAEFINV--TTRVWNRFPAASTGTQVQ 1090
Qy      1051 LCGSLISIFNSKGFHLVGSNLSIAQVVMKVYVERKOMLYLVYLSG--IGALLLLILF 1108
Db      1091 LTTAAABIDTNPQFLVIBENAVTIPIMINKPT---EKAEVPTGVITIGSIAGILLIANT 1147
Qy      1109 IVLYKVGFFKRNKKE 1123
Db      1148 AGLMKLGFFKRYKQ 1162

```

```

RESULT 12
158409
Integrin alpha-9 chain precursor - human
C/Species: Homo sapiens (man)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: 158409; A49459
R/Hibi, K.; Yamakawa, K.; Ueda, R.; Horio, Y.; Murata, Y.; Tamari, M.; Uchida, K.; Takah
Onogene 9, 611-619, 1994
A/Title: Aberrant upregulation of a novel integrin alpha subunit gene at 3p21.3 in small
A/Reference number: 158409; MUID:94119603; PMID:8290272
A/Accession: 158409
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1035 <RES>
A/Cross-references: UNIPROT:O13797; GB:D25303; NID:9464180; PDB:BA04984.1; PID:9533327
R/Palmer, E.L.; Ruegg, C.; Ferrando, R.; Pytela, R.; Sheppard, D.
J. Cell Biol. 123, 1289-1297, 1993
A/Title: Sequence and tissue distribution of the integrin alpha9 subunit, a novel partne
A/Reference number: A49459; MUID:94064789; PMID:8245132
A/Accession: A49459
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 30-1035 <PAL>
A/Cross-references: GB:L24158
C/Keywords: glycoprotein; metal binding; transmembrane protein
F/1-27/Domain: signal sequence #status predicted <SIG>

Query Match 11.1%; Score 678.5; DB 2; Length 1035;
Best Local Similarity 23.1%; Pred. No. 2,5e-38;
Matches 289; Conservative 190; Mismatches 391; Indels 381; Gaps 53;

QY 22 PASYNLDVGARSPSPRAGHFGYRYLVQVNG-----VIYVAPGEGN-----STGSL 70
DB 26 PAGAYNLDVQPVHFGP-ADSFEGYAVLHFDHTRWLVGAPADSKYSPSPVSPAV 84
QY 71 YQCGSGT---HCLPVTL-RGSN-----YTSKYLGMTLATP-TDGSILADP 113
DB 85 FKCRVHTPDRCTELDMARGNKRGTSCKTCREDDEMMGVSLARPKADGVTACAH 144
QY 114 GLSRTCDONTYLS-----GLCYLFRONLQPMLOGR---PGFQECIKGNVDLVFLDG 163
DB 145 RM-----KRIYEAHHLPHGFCYIIPSNLQ--KSKTLLPCYE----- 182
QY 164 SMSLOPDEFQKILDFMKDVMKKLSNTSYQFAVQPSYKTEFDFSDYKRDPAALKH 223
DB 183 -----YKKKYG----- 188
QY 224 VAKMLLNTFGAIVYATEVFRBELGAPDPTKVLITTDGEATSGNIDANDIIRYI 283
DB 189 -----EEHGS----- 193
QY 284 IGIGHFQTKESQETLHKFAPKAPSEFKLIDTFEKLKDLFTELQKTIYVIGTSKQULT 343
DB 194 ----- 193
QY 344 SFNNELSSSGISADLSRGHAAVAVGAKDWAGFGFLDKADLDDPTFIG-NEPLTEPVAG 402
DB 194 -----CQAGIAGFTBELVVMGAGSRYWAGTIKVL--NLTDNYVLKLBVIMNRYT 245
QY 403 YLGIYVT-WLPSRQKTSLSLGAAPYQIMGRVLLFOEPQGGHMSOVOTIHGTQIGSYFG 461
DB 246 YLGIYVTAGHFSHPSTIDVVGAPQDKIGIKYIIFRARRSGSTLLKIFQASGKMGSYFG 305
QY 462 GELGVNDVQDGETELLIGAPLFGEGQRGAPVFIYQROG-PEEVELGDDPPYRGR 520
DB 306 SLLCAVDLADGDLSD-LIVGAPMSEIRDEGQVTVYIRNGKALBESQALTGDAVN-AH 363
QY 521 FGEATITLTINGDGLVDVAVGAPLEEQ--GAVYIFNGHGGISLPQSPQRTGCTVLSGI 578
DB 364 FGEISLSDLDLNDGFPDVALIGAPKEDDPAGAVVYIHGDAGGIIVQYMKKSGQKINVL 423
QY 579 QMFGSHGVNDLBDGDLADVAVGA--ESQMTLVSSRPVDMVTLMSPSPAIPIVHAEVC 636

```

```

DB 424 RMFGQISISGIDMDNGNPPVTVGAFMSDSVLLRARFVI-TVYVSLFPLRESITITPQC 482
QY 637 SYSTSNKRGKGNVITTCFQIKSLYPOFQRLV--ANLYTTLQDGHRTRRGLP---- 689
DB 483 --HDGQPPVNCIANTGCF-----SFHGKVPBEIGLANYLMDVAK-KKQGMPIRYF 532
QY 690 ----GGHELRNIAVY-TSMSCITDPSFHPVVCYODLISPIVNSLANSIMEESTPPDR 744
DB 533 VLIGETVQVTEKQLQITMEETCHYVAHVARRQDVISPVEBAASL-SEHYTGBER 591
QY 745 AQGDPIPLRPSLH-----SETWEIPFEKN-----CGEDKCEANLRFSPASRA 792
DB 592 ----ELRP-LTPVLRMKKGKIAQKQTVFERKRSRSDCAADLQGLKLLSDEKTYL 646
QY 793 LRLTAFAASLSELSLNEBDAYVVDLHFPPLSLF---RKVEMLKPSHQPVSCEEL 848
DB 647 LALGAVNIGISLISNIGDADYDANVSFNVSRLEFPINMWQKEM-----DISCEL 699
QY 849 PEESRLSRALSCNVSSPIFRAGSHVALQMMFNTLVNSMGDSVELHANTYC--NNEDS 905
DB 700 E-----SDFLKCSGVGFPMRSKSKYFESVYFDTSHLS--GEERVLSPITYAOGSNTERS 751
QY 906 DLLEDNSATTIPLIYPIINLILQDQEDSTLYSFTPKGPKIHQY-----HMVQR 956
DB 752 ESLHDNTLVLMPLMHEVDTSITGIMSPSTFV---YGESVDANFIQLDDLECHFOPI 807
QY 957 IQPSIHD---HNITPLAAVGVQPPSECPITTHQMSVQ-----MEPPVPC- 998
DB 808 ITLQVNTGPTLPLDSSVSISFPRRLSSG-ALMFHYQEMVVGQKNGCRQKPTFCII 866
QY 999 --HYEDL-----ERLPDAEPCLPGLFRC-PVFERQ--ILVQVITLTEL 1039
DB 867 PQEENIFHTIFAFETKGRKVLDCERKGISCLTAHCNPSALAKESRTIDYMLNTEI 926
QY 1040 VGETEASMSLSGSLSSISRNSS-KHFLYGSNLSLAQVMKVUVYK-----QM 1089
DB 927 LKR-DSSSVIQFMSRAKVADPALVVEIAHGNE-----EVYVEALHNTLPRGYV 979
QY 1090 LYLVLVSGIGLILLILLIYLYVYVGFKNLKEKMEAGRVPGIAPDS 1140
DB 980 GMITAILVGIILFLLAVLVMCMGFFRRRYKIIIEAK--NRKENEDS 1027

RESULT 13
A41131
Lymphocyte-Peyer's patch adhesion molecule alpha 4 precursor - mouse
N/Alternate names: Integrin alpha-4
C/Species: Mus musculus (house mouse)
C/Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 09-Jul-2004
C/Accession: A41131; S16742
R/Neuhaus, H.; Hu, M.C.T.; Hemler, M.E.; Takada, Y.; Holzman, B.; Weiseman, I.L.
J. Cell Biol. 115, 1149-1158, 1991
A/Title: Cloning and expression of cDNAs for the alpha subunit of the murine lymphocyte-1
A/Reference number: A41131; MUID:92064645; PMID:1840602
A/Accession: A41131
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1039 <NEU>
A/Cross-references: UNIPROT:Q00651; EMBL:X53176; NID:951484; PDB:CAA37316.1; PID:951485
C/Superfamily: Integrin alpha-4 chain
C/Keywords: cytoskeleton; transmembrane protein

Query Match 10.4%; Score 633; DB 2; Length 1039;
Best Local Similarity 23.4%; Pred. No. 3,6e-35;
Matches 285; Conservative 193; Mismatches 425; Indels 316; Gaps 54;

QY 6 ITVMAMALLSGFEFPASSYNLDVGARSPSPRAGHFGYRYLVQVNG-----VIYVAP 61
DB 21 IALREAVMLLYFGVPTGSPSYNLDPENALLYQGP-SGTLFGYSVVLHSHSKRWLIYVAP 79
QY 62 GEGNSTGSLVQCGSGTGHCLPVTLRGSNTSKYLGMTLATDPTDGSILADPGL-----SR 117

```



```
Db 80 -----TASWLSNAGVNP--GAIYRC--GIKRNPNQ 106
Qy 118 TCDQNTYLSGLCYLFRONLQGPMLQGRPGFOEICKANVDLVELFDGSMLSLPDEROKLTD 177
Db 107 TCBO-----LQSGSPGEGPCGKTCLEER-DNQWL-GYTISRPGENGSL-- 148
Qy 178 FMKQVMKLSNTSYQFAAVPSTSYKTEFDFSDYVK--RKDPDALLKHVKMLLTNTFG 235
Db 149 -----VTCGHRWKNIF--YKSDNKLPT----- 169
Qy 236 AINVAATEVPREELGARDATKULIITIDGATSDGNDAKDRIYIIGIKHFQYKES 295
Db 170 GICVYMPEDLRTLSKR-----MAPCYKDYR----- 196
Qy 296 QETLHKFASPKASEPVKILDTFEKLKDLFTELOKKIYIEGTSKQDLTSFMNMLSSSGIS 355
Db 197 -----KREBNPAS-----CQAGIS 210
Qy 356 ADLSRGHAVVAGVAKDMAGG-FLDLKADLDDTFIGNEPLTPEVYRAG-YLGATVYVWLPIS 413
Db 211 SFYIODLIVMGAPGSSYWTGTVFVYVNTTNQYKAFVDRQ---NQYKFGSYLGYSVGAHF 267
Qy 414 RQ-KTSLASGAPRYQHMGRVULFOEPGCGGHSQVOTIHGTQIGSYFGELCGVDVDQD 472
Db 268 RSPHTTEVVGAPQHBOIGKAYIFSIDE--NELNIVYEMKKGKLGSGYASVCAVDLNDAD 325
Qy 473 GETELLILGADLFYGEORGRGVFIYORQLG---FEVSELSQDGPYGLGRFEALTYLT 529
Db 326 GFSD-LIVGAPMOSITIREGRVFIYINGMGAVVEMERVLVGSKY-AAAFGESIANLG 383
Qy 530 DINGDGLVAVAPLEB--QGAAYIFNGRHGGLSPQSORIEGTQVLSGIQWFGRSIHG 587
Db 384 DIDMGFEFDIAIGAPQBDLRGAVYIYNGRVDSISSTYQRIEGQIISKLRMGQGSISG 443
Qy 588 VKDLBGGLADVAVCA--ESQMITVLSRPVVDMTLMSFSPAELPVHVECSYSTSNKMK 645
Db 444 QIDDMNNGYVAVAGAFQSDSAVLLTRTPVVIIVASLS-HPESVNRTKFDG--TENGLP 499
Qy 646 E-GVNTITFOIKSLYPOFQGRVLANLYTTLQDQHR---TRRRGLPFGGRHE-LRNRI 699
Db 500 SVCHNLITLCSYKQ--KEVPGYIV-LFTVNSLDVHRAEBSRKYFFSNTSDVITGSI 555
Qy 700 AVTTS-MSTDPFSHFVPCVODLISPIVNSLNFSLMEBEGTPRDQAGKDIPIPLRPSL 758
Db 556 RVSSSGEKCTHQAFMRKQVDILTRIVHATYHLGHVITKRNK---EEFPP-LQDPL 610
Qy 759 HSEFWB-----IPEKKGCEDEKCCENLRYS---FSPKRSRA-LRLTLPASLSVELS 806
Db 611 QOKKEKQVIRKMINFARPCAYE-NCSADLVSAKVGLPKPYENTYILAVGSMKTIAMNVS 669
Qy 807 LSNLEBDAYVQOLDHPFPGLSFRKVBMLKPHSQIPVSCCELPPESRLLSRALSQVSSP 866
Db 670 LFMAGDDAYETTLNVQLFTGTYFIKILDL--EKQINC-EVTSSSGIVK--LACSGLGYI 723
Qy 867 IFKAGHSVALQOMENRTLVNSWGDSEVELHNAVYTCNNE--DSDLEBNSATITIIPIIYPINI 925
Db 724 YVDRLSRIDISFLDVSLSRAHEDLSISVASCENBEGELDQVNDRTLTILPIRYEMML 783
Qy 926 LIQOQEBSTLYV-----SFTPKGPKIHQVKMYOVRLOPSJHDHNIPTLBAVGVQ 977
Db 784 TVHGLVNTSPFVYSSSENEBETCMABKDLNLFVINTGISMA-----PWSYKIMWPN 837
Qy 978 P--PSEGPITHQMSVQMPRPVPCYEDLERLPDAABPCLPGLPRCPVPVFOELIVQYIG 1035
Db 838 SFLPQDDGLFVNLVDQTTG-QCHFKAQR-----ECTPAQCKGIAGLTLD 882
Qy 1036 TLELVGETEASMSL-----CSSLSISF-----NSSKPFHLYG-----SNASIAQ 1076
Db 883 IVKFLSKTDKRLYCMKADQHCPLCNFGMGSGSKASVHIQLEGRSIEMEMETSIX 942
Qy 1077 VVMK-----VDVYVEKQMLLYV-----LSGIGILLILLI 1107
Db 943 FEIKATAPPEBPHKVIIBLNQDENAVHVLBGLHHQRPKRHFTIITITISLGLIIVLLI 1002
```

```
Qy 1108 FIVLYKVPFKRNLEKME 1126
Db 1003 SCVMMKAGFFKRYQKSLIQ 1021

RESULT 14
506046
Integrin alpha-4 chain precursor - human
N:Alternate names: CD49d; very late antigen-4 alpha chain; VLA-4 alpha chain
C:Species: Homo sapiens (man)
C:Date: 01-Dec-1989 #sequence, revision 01-Dec-1989 #text_change 09-Jul-2004
C:Accession: 506046; A39355; D28018
R:Takada, Y.; Ellices, M.J.; Crouse, C.; Hemler, M.E.
EMBO J. 8, 1361-1368, 1989
A:Title: The primary structure of the alpha(4) subunit of VLA-4: homology to other integr
A:Reference number: 506046; MUID:89356603; PMID:2788572
A:Accession: 506046
A:Molecule type: mRNA
A:Residues: 1-1038 <TAK>
A:Cross-references: UNIPROT:P13612; GB:X16983; EMBL:X15356; NID:g33945; PIDN:CAA34852.1;
R:Rosen, G.D.; Birkenmeier, T.M.; Dean, D.C.
Proc. Natl. Acad. Sci. U.S.A. 88, 4094-4098, 1991
A:Title: Characterization of the alpha-4 integrin gene promoter.
A:Reference number: A39355; MUID:91239513; PMID:2034655
A:Accession: A39355
A:Molecule type: DNA
A:Residues: 1-93 <ROS>
A:Cross-references: GB:M62841
R:Takada, Y.; Strominger, J.L.; Hemler, M.E.
Proc. Natl. Acad. Sci. U.S.A. 84, 3239-3243, 1987
A:Title: The very late antigen family of heterodimers is part of a superfamily of molecu
A:Reference number: A94151; MUID:87204112; PMID:3033641
A:Accession: D28018
A:Molecule type: Protein
A:Residues: 40-50; 'E', 52-53 <TA2>
A:Genetics:
A:Gene: GDB:ITGA4; CD49D
A:Cross-references: GDB:128032; OMIM:192975
A:Map position: 2q31.2q32
C:Keywords: Integrin alpha-4 chain
C:Keywords: cell adhesion; cytoskeleton; duplication; glycoprotein; heterodimer; transmem
F:1-39/Domin: signal sequence #status predicted <SIG>
F:40-1038/Product: Integrin VLA-4 alpha-4 chain #status predicted <MAT>

Query Match 10.1%; Score 619.5; DB 2; Length 1038;
Best Local Similarity 25.9%; Pred. No. 3.1e-34;
Matches 235; Conservative 168; Mismatches 337; Indels 169; Gaps 44;

Qy 322 DLFTLEOKKIYVLEGTSKOD-LTSFMNELSS--SGISADLSRGHAVVAGVAKDMAGFL 378
Db 177 DLRTLELSKRI-----APFYQDYVKKFGENFASCGAGISSFTTKOLIWMGAFGSSYWTGSLF 232
Qy 379 -----DLKA--DLQDPTFIGNEPITPEVYRAGLYGVYVWLPISR-QKTSLSAGAPRYQ 428
Db 233 VYNTITTKYKAFPLDKQNVFGS-----YLGYSVGAHFRRQHTTEVVGAPQH 282
Qy 429 HMGVULLFOEPGCGGHSQVOTI---GTQIGSYFGELCGVDVDQDGETELLILGAPLE 485
Db 283 QIGKAYIFSIDE-----KELNIIHEMKKGKLGSGYASVCAVDLNDGFSQD-LLVGAPMQ 336
Qy 486 YGEORGRVFIYORQLG---EEVSELSQDGPYGLGRFEALTYLTIDINGDGLVAVAG 542
Db 337 STRREGRVFIYINGMGAVVEMERVLVGSKY-AAAFGESIYNLQDIDNDGFEVDYATG 395
Qy 543 APLEB--QGAAYIFNGRHGGLSPQSORIEGTQVLSGIQWFGRSIHGVVDLREGDGLADVA 600
Db 396 APQEDDLQGAIVLYNGBADGISSTFGQRIEGLDISLSMFGGSIQGDADANNQGYVDA 455
Qy 601 VCA--ESQMITVLSRPVVDMTLMSFSPAELPVHVECSYSTSNKMEG-----VNTITC 653
Db 456 VGFARSDSAVLLTRTPVVIIVDASLS-HPESVNRTKFDG-----VENGPVSCIDLITLC 507
```



QY 654 FOIKSLYPOFOGRVLAANTLYTLQDGHRTTR---RGLFP---GGRHELRNIAVTT-SMSC 707  
DB 508 FSYKG--KEVGYI--LFTNMSLDVNRKABSPFPYSSNCTSVITGSLQVSSREANC 563  
QY 708 TDFSHFPVYVODLISPINVSINFSLMBEGTPRDQAOQKDIPILRPSLHSETWE--- 764  
DB 564 RTHQAFMKQVDILTIPIQIEAAHYL---GPHVSKRSTEEFP-LQPILOQKKEXDIM 618  
QY 765 ---IPEKKGCEDEKCEANLRY---FSPARSA-LRLTAFASLSVELSLNEDAY 815  
DB 619 KKTINFAPFCAHE--NCSADLQVSAKIGFLKPHENTYLA VGSMTLMLNVSLFNAGDAY 677  
QY 816 WYQDLHPPGLSPEKVEMLKPHSQIPVSCCELPEBSLLSRALSQVSSPIFKAGSVA 875  
DB 678 ETTLVKLPVGLYFKILIELE---EKQINC-EVTNNGVQ--LDCSIG--YIYDHLR 729  
QY 876 LQMMF---NTLVNSWGDVVELAHANVCNNEDS--DLLEDNSATTIIPILPINILIOD- 929  
DB 730 IDISFLVSVSLSRABEDSLTVHA--TCENEBENDLKHSHVYVAIPLKTEVKLTVAHG 787  
QY 930 -QEDSTLYVSTPQPKIHQVKMYQVRIQPSIHDNIPTLEAVVGPQ--PPESGPITH 986  
DB 788 VNPFSFVYGSNDENPEFCWVEKMLTFHVINTGSMAPNVSVETMVPNSFSPQDKLFN 847  
QY 987 QMSVMEBPVPCHYEDLEBLPDAAPCLBGLFRCPVVFRQELIVQVGTLEVEITAS 1046  
DB 848 ILDVOTTTG-BCHFNHYQRV-----CALBOQKSNMOTLKGIVAFISKTDR 892  
QY 1047 SMFSL-----CSSLSISF-----NSSKHFLYSG----- 1069  
DB 893 LLYCTKADPHCLNFCNGKMGESGEASVHTQBERPSILEMDETSALKFEIRATGPEP 952  
QY 1070 -----SNASLAQVNRKDVVYERQMLYLYVL---SGIGGLLLLLLIFIVLYKGVF 1117  
DB 953 NPRIVELKNDENVAVHLE-GLHQRPKRYFTIIVISSLLGLIVLLISVVMKAGFF 1011  
QY 1118 KRNLEKME 1126  
DB 1012 KRQYSLIQ 1020

RESULT 15  
T31437  
Integrin alpha chain SU2 - sea urchin (Lytechinus variegatus)  
C:Species: Lytechinus variegatus (variegated urchin)  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T31437  
R:Hertzler, P.L.; McClay, D.R.  
submitted to the EMBL Data Library, May 1998  
A:Description: Alpha SU2, a sea urchin integrin which binds laminin.  
A:Reference number: 221035  
A:Accession: T31437  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1041 <HR>  
A:Cross-references: UNIPROT:O76378; EMBL:AF067658; NID:G3220240; PID:G3220241; PIDN:AAC2  
A:Experimental source: developmental stage embryo  
A:Function:  
C:Superfamily: Integrin alpha-2b chain

Query Match 9.6%; Score 588; DB 2; Length 1041;  
Best Local Similarity 22.5%; Pred. No. 4.7e-32;  
Matches 289; Conservative 199; Mismatches 407; Indels 392; Gaps 61;

QY 9 MAMALLSGFF---FAPASVNLIVRGARSPFPAGHFGYRVQVNG---YVIGAP 61  
DB 1 MARILLISFYAILLDSTAGFNFDLAPLKFDGP-DGSMFGSVAQHRDGNTDWALVAP 59  
QY 62 -----GEGNSTGSLYOCOSGTGHC--LPTVLRG---NTYSKYLGMTLATDPTDG 106  
DB 60 EASTNOSGVTGKGA VYSCRPISGSPVCEQIIPFDKGTGINNVNDKSNQMGFATVASGANG 119

QY 107 SILACDPGLSRTCDQNTYLSGLCYLFRONLQGPMLQGRPGHQEICKGNVDLVPFLPDSMS 166  
DB 120 QILMLCARFL-----VWVETASVTRKQREBPFGTFFVGDSD---FTMFVN 160  
QY 167 LQDPEFOKILDFMKDVNKKLSNNTSYOPAAVOFSTSYTEPDPFDYVRKRPDALLKHYKH 226  
DB 161 YSPQSTNRREDYGD---KITHQAGFSGLIFS-----DMSALV----- 196  
QY 227 MLLTLTTFGALNVYATEVFEBELCAPDPATKVLIIITDGEATDSGNIDAKDITRIYIGI 286  
DB 197 -----MGA----- 199  
QY 287 GKHPQTKBSQETLHKFASKPASEPVKILDPFEKULFTELQKKY-----YIBGTS 338  
DB 200 -----PestY-----LQGIYVQSLNRSVQATQ 224  
QY 339 KQDLTSFMNELSSSGISADLSRGAHVAGAKDMAGGFLDKKADLDDPTFGNEPLRPE 398  
DB 225 ESNVTGTSFDSYNGYSLALG-----DFND----- 250  
QY 399 VRAGYLYTWTLPBSROKTSILSAGAPRYQH-MGRVLLPQEPQGGHNSQVQTHGTQIG 457  
DB 251 ---GVQYVV-----GTPRASELMGLVAFDQ---NLNQFNQVWGQIY 288  
QY 458 SYRGEELGCVVDQDGETELLIGAPLYGB---QR--GGRVPIY-QRQLG-----F 504  
DB 289 AYPGYSVTVVDINDTYDD-LVGAPEYMDGPALQWMAAVALVYIQNPVGGASNL 347  
QY 505 BEVELQODPGYPLGRFGEATITALTIDNGDLVAVAGAPLE--EQGAVYFNGRHGLS 562  
DB 348 SLSTSLIG--QIHSRKGSLASIGDSNQGFNDVAILGAPREGDAGAVYIYHSANGLK 405  
QY 563 POPSQRI-BGTQVLSGIQWFGRSIHGVKDLGEGDLADVAVGAE--QMTVLSRPVYDMV 619  
DB 406 STPAQVLTPLSLGSHGITTFFGFSLQGGQDMKNKYPDLVAGSANTAVAILRTRPVVSLD 465  
QY 620 TLMSPSAELPVHVEBSYSTSNMKEGVNIT-----ICPQIKSLY-PQPGRLVANLTY 673  
DB 466 ATLNTPEPGLNLE-----NKTVELADGTWTSFIAMTCFTYTGNYLBDH-----IDISY 514  
QY 674 TLQD-GHRTTRRGLF-PGGRHEL--RNRNAVTTSMSCDPSFHPVPCVODLISPINSL 729  
DB 515 TVTVDSGLIANRKAMFVNDMSIETKTRRLAVSTQF-CDPLRAYVGSIEBKLTPIKTYL 573  
QY 730 NFSLMWEGTPRDQAOQKDIPIL-RPSLSHSETWEIPEKNCGEDEKCEANLVSFSPA 788  
DB 574 QYDLNND-----SRLOPHETLPIIDMATSTQKQVSIQNC--VNNICIPDLDTVYTPN 627  
QY 789 RSRALRLTAFASLSVELSLNLEDAVWQDLHPFGSLFRKVEMLKPHSQIPVSCCEL 848  
DB 628 LPNTIV-IGQTOELTLDVSLNNRGEAFQSSLSVYPPGLQFVRLER-KANMDFSVTCS-- 683  
QY 849 PERSRLSRALSQVSSPIPKAGHSV-ALQMMFPTLVNSMGDSVELAHANVTC--NNESD 906  
DB 684 -EDSDL--RIITCTGNPM--VGKNILFEGTLTSPVSGDKDSIEYFPKASENSBDPN 738  
QY 907 LLEBNSATTTIIPIL-----YPINILIQDEBSTLYVSTPQPKIH----- 947  
DB 739 TLENNELMNTVYPVAVDCTLKLKLSAYBEIYWSQED---YV--VPPFPANASBADIGM 793  
QY 948 QVKMYQVRIQPSIHDNIPTLEAVVGPQPPSEGP-ITHQMSVQMEBPVPCHYEDLERL 1006  
DB 794 EVMHLYEVR--NTGSSNAGVSLNIIQMPQKNBDEGVLYFYLLGIMTEBQVYCOLTOGKAN 850  
QY 1007 PDAA--EPC-----LPGALFRCPVVFRQELIVQVGTLELVEITASMFSLCS 1053  
DB 851 PEGYKLEPSTKAKLSNNTTQVSGKRKEPEV--AEALAQIDNVYTCASD---SCVLIINCT 905  
QY 1054 SLGISFNSSKGFLHYG-----SNASIAQVVMKVDV----- 1083  
DB 906 IDEINASKSKVRIILGFRWERTFOKAVSELTPVQVQATIASASAIVKTIIPYNIPLPDPFS 965  
QY 1084 -----VYEKQML-----YLYVLSGIGILLILLIFIVLYKXGFPFRNLEKEMEA 1127

Db	966	DSTKASTLVTTBELVPPVTPIAMWIIVSVLGIIILLLIIIGLWKCGFPERKK-----	1019
OY	1128	GRGVNNGIPAEDE--OLASGOEAGDP	1152
Db	1020	-----PGEKEAYAPVASADKOGPF	1038

Search completed: August 29, 2005, 19:24:24  
Job time : 37 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 29, 2005, 19:12:58 ; Search time 114 Seconds  
(without alignment)

5255.550 Million cell updates/sec

Title: us-09-945-265-2

Perfect score: 6106

Sequence: 1 MKDSCITMANALLSGFFPP.....DPGLKPLHKKDSGSGGKD 1170

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6106	100.0	1170	1	ITRA1_HUMAN
2	5585	91.5	1086	2	Q96HBI
3	4657.5	76.3	1165	1	ITRA1_BOVIN
4	4571.5	74.9	1166	2	Q6TYB8
5	4365.5	71.5	1161	2	Q9WTVA
6	4361	71.4	1160	2	Q9R200
7	4343.5	71.1	1163	1	ITRA1_MOUSE
8	3644.5	59.7	927	2	Q8H2V0
9	1583.5	25.9	1188	2	Q6KAS4
10	1582.5	25.9	1169	1	ITAX_MOUSE
11	1562.5	25.6	1152	1	ITAX_MOUSE
12	1526.5	25.0	1163	1	ITAX_HUMAN
13	1516	24.8	1161	1	ITAX_HUMAN
14	1514.5	24.8	1153	1	ITRM_MOUSE
15	1488.5	24.4	1151	2	Q9J130
16	1476	24.2	1162	1	ITAD_HUMAN
17	1442.5	23.6	1187	2	Q98TF0
18	1436.5	23.5	1196	2	Q98TF1
19	1243	20.4	920	2	Q28984
20	1154	18.9	1189	1	ITAH_HUMAN
21	1121	18.4	1188	1	ITAH_MOUSE
22	1118	18.3	1188	2	Q7TQC3
23	1114.5	18.3	1151	1	ITAI_HUMAN
24	1112.5	18.2	1180	1	ITAI_HUMAN
25	11105	18.1	1167	1	ITAG_HUMAN
26	1070.5	17.5	269	2	Q80WE9
27	1012.5	16.6	1170	1	ITAZ_BOVIN
28	1007.5	16.5	1167	2	Q88341
29	995	16.3	1167	2	Q88340
30	994	16.3	1171	2	Q42094
31	993	16.3	1167	1	ITAE_MOUSE

32	985	16.1	1181	1	ITRA2_HUMAN	P17301 homo sapien
33	976.5	16.0	1179	1	ITAE_HUMAN	P38570 homo sapien
34	959	15.7	1178	1	ITAZ_MOUSE	Q62469 mus musculu
35	959	15.7	1178	2	Q6PIC7	Q6PIC7 mus musculu
36	907.5	14.9	1038	2	Q8BS01	Q8BS01 mus musculu
37	894.5	14.6	895	2	Q9WU8	Q9WU8 mus gp. itg
38	872	14.3	1160	2	Q8MKR4	Q8MKR4 felis alive
39	803	13.2	823	2	Q8WY18	Q8WY18 homo sapien
40	765.5	12.5	823	2	Q8CE84	Q8CE84 mus musculu
41	754.5	12.4	1332	2	Q9BPQ8	Q9BPQ8 halocynthia
42	679	11.1	1036	2	Q91YD5	Q91YD5 mus musculu
43	678.5	11.1	1035	1	ITRA9_HUMAN	Q13797 homo sapien
44	668.5	10.9	780	2	Q06271	Q06271 xenopus lae
45	633	10.4	1039	1	ITRA4_MOUSE	Q00651 mus musculu

#### ALIGNMENTS

RESULT 1

ID	ITRA1_HUMAN	STANDARD	PRT	1170 AA.
AC	P20701: Q43746; Q9UBC8;			
DT	01-PEB-1991 (Rel. 17, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Integrin alpha-L precursor (leukocyte adhesion glycoprotein LFA-1 alpha chain) (CD11a).			
DE	Name=ITRA1; Synonyms=CD11A;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1), AND PARTIAL SEQUENCE.			
RA	MEDLINE=89139587; PubMed=2537322; DOI=10.1083/jcb.108.2.703;			
RA	Larson R.S., Corbi A.L., Berman L., Springer T.;			
RT	"Primary structure of the leukocyte function-associated molecule-1 alpha subunit: an integrin with an embedded domain defining a protein superfamily.";			
RT	J. Cell Biol. 108:703-712(1989).			
RL	[2]			
RN	SEQUENCE FROM N.A. (ISOFORM 2).			
RP	MEDLINE=99425270; PubMed=10493829; DOI=10.1006/geno.1999.5927;			
RA	Loftus B.J., Kim U.-J., Sneedon V.P., Kalush F., Brandon R.;			
RA	Puhmann U., Mason T., Crosby M.L., Barnstead M., Cronin L.;			
RA	Deblatere Mays A., Cao Y., Xu R.K., Kang H.-L., Mitchell S.;			
RA	Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;			
RT	"Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q.";			
RT	Genomics 60:295-308(1999).			
RL	[3]			
RP	SEQUENCE OF 1-20 FROM N.A.			
RA	MEDLINE=93281759; PubMed=8099450;			
RA	Shelley C.S., Farokhzad O.C., Arnaout M.A.;			
RT	"Identification of cell-specific and developmentally regulated nuclear factors that direct myeloid and lymphoid expression of the CD11a gene.";			
RT	Proc. Natl. Acad. Sci. U.S.A. 90:5364-5368(1993).			
RL	[4]			
RP	SEQUENCE OF 1-20 FROM N.A.			
RA	MEDLINE=93374910; PubMed=8103515;			
RA	Nueda A., Lopez-Cabrera M., Vara A., Corbi A.L.;			
RT	"Characterization of the CD11a (alpha L, LFA-1 alpha) integrin gene promoter.";			
RT	J. Biol. Chem. 268:19305-19311(1993).			
RL	[5]			
RP	SEQUENCE OF 1-20 FROM N.A.			
RA	Pubmed=8097887;			
RA	Cornwell R.D., Gollahan K.A., Hickstein D.D.;			
RT	"Description of the leukocyte function-associated antigen 1 (LFA-1 or CD11a) promoter.";			

```

RL Proc. Natl. Acad. Sci. U.S.A. 90:4221-4225(1993) .
RN [6]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 153-335, AND REVISION TO 214.
RX MEDLINE=96036067; Pubmed=7479767;
RA Qu A., Leahy D.J.;
RT "Crystall structure of the I-domain from the CD11a/CD18 (LFA-1, alpha L
beta 2) integrin.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:10277-10281(1995) .
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 153-335.
RX MEDLINE=96396882; Pubmed=8805579; DOI=10.1016/S0969-2126(96)00100-1,
RA Qu A., Leahy D.J.;
RT "The role of the divalent cation in the structure of the I domain from
the CD11a/CD18 integrin.";
RL Structure 4:931-942(1996) .
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 153-334.
RX MEDLINE=99425288; Pubmed=10493852; DOI=10.1006/jmbi.1999.3047;
RA Kallen J., Weizsaeck K., Rammge P., Geyl D., Kriwacki R., Legge G.,
RA Cottenes S., Weitz-Schmidt G., Hommel U.;
RT "Structural basis for LFA-1 inhibition upon Iovastatin binding to the
CD11a I-domain.";
RL J. Mol. Biol. 292:1-9(1999) .
CC -I- FUNCTION: Integrin alpha-L/beta-2 is a receptor for ICAM3, ICAM2,
ICAM3 and ICAM4. It is involved in a variety of immune phenomena
including leukocyte-endothelial cell interaction, cytotoxic T-cell
mediated killing, and antibody dependent killing by granulocytes
and monocytes.
CC -I- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-L
subunit associates with beta-2.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=1;
CC -I- IsoId=P20701-1; Sequence=Displayed;
Name=2;
CC -I- IsoId=P20701-2; Sequence=VSP_002738;
CC -I- Note=No experimental confirmation available;
CC -I- TISSUE SPECIFICITY: Leukocytes.
CC -I- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins
with I-domains do not undergo protease cleavage.
CC -I- SIMILARITY: Belongs to the integrin alpha chain family.
CC -I- SIMILARITY: Contains 7 FG-GAP repeats.
CC -I- SIMILARITY: Contains 1 VWFA domain.
CC -I- SIMILARITY: Contains 1 VWFA domain.
CC -I- DATABASE: NAME=PROV; NOTE=CD guide CD11a entry;
WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd11a.htm".
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch) .
CC
DR EMBL; Y00796/ CAA68747.1; -
DR EMBL; AC002310; AAC31672.1; -
DR EMBL; M95609; AAA16474.2; -
DR EMBL; Z22804; CAA80461.1; -
DR EMBL; M87662; -; NOT ANNOTATED_CDS.
DR PIR; S03308; S03308.
DR PDB; 1COP; X-ray; A/B=153-334.
DR PDB; 1DGO; NMR; A=149-336.
DR PDB; 1LFA; X-ray; A/B=-.
DR PDB; 1MCN; X-ray; A=153-331.
DR PDB; 1MO8; X-ray; B/D=155-331.
DR PDB; 1MO9; X-ray; A=152-330.
DR PDB; 1MOA; X-ray; A=152-330.
DR PDB; 1ZON; X-ray; A=150-336.
DR PDB; 1ZOO; X-ray; A/B=150-336.
DR PDB; 1ZOP; X-ray; A/B=150-336.
DR GeneW; HGNC:6148; ITGAL.
DR Mim; I53370; -

```

DR	GO: 0008305; C:integrin complex; TAs.	
DR	GO: 0006928; P:cell motility; TAs.	
DR	InterPro; IPR000413; Integrin_alpha.	
DR	InterPro; IPR002035; VWF_A.	
DR	Pfam; PF01839; FG-GAP; 3.	
DR	Pfam; PF00357; Integrin_alpha; 1.	
DR	Pfam; PF00092; VWA; 1.	
DR	PRINTS; PR01185; INTEGRINA.	
DR	PRINTS; PR00453; VWFADOMAIN.	
DR	SMART; SM00191; Int_alpha; 5.	
DR	SMART; SM00327; VWA; 1.	
DR	PROSITE; PSS00242; INTEGRIN_ALPHA; 1.	
DR	PROSITE; PSS0234; VWA; 1.	
KW	3D-structure; Alternative splicing; Calcium; Cell adhesion; Direct protein sequencing; Glycoprotein; Integrin; Magnesium; Receptor; Repeat; Signal; Transmembrane.	
KW	Receptor; Repeat; Signal; Transmembrane.	
FT	SIGNAL	1 25
FT	CHAIN	26 1170
FT	DOMAIN	26 1090
FT	TRANSMEM	1091 1111
FT	DOMAIN	1112 1170
FT	REPEAT	412 91
FT	REPEAT	92 149
FT	DOMAIN	156 327
FT	REPEAT	350 400
FT	REPEAT	401 455
FT	REPEAT	457 516
FT	REPEAT	518 575
FT	REPEAT	578 630
FT	CA_BIND	468 476
FT	CA_BIND	530 538
FT	CA_BIND	590 598
FT	SITE	1115 1119
FT	DISULFID	73 80
FT	DISULFID	111 129
FT	DISULFID	653 707
FT	DISULFID	771 777
FT	DISULFID	845 861
FT	DISULFID	998 1013
FT	DISULFID	1021 1052
FT	CARBOHYD	65 65
FT	CARBOHYD	85 89
FT	CARBOHYD	188 188
FT	CARBOHYD	649 649
FT	CARBOHYD	670 670
FT	CARBOHYD	726 726
FT	CARBOHYD	730 730
FT	CARBOHYD	862 862
FT	CARBOHYD	885 885
FT	CARBOHYD	897 897
FT	CARBOHYD	1060 1060
FT	CARBOHYD	1071 1071
FT	VARSPLIC	954 954
FT	CONFLICT	214 214
FT	CONFLICT	660 660
FT	STRAND	155 162
FT	STRAND	164 164
FT	TURN	165 166
FT	HELIx	169 185
FT	TURN	186 188
FT	STRAND	191 198
FT	STRAND	202 206
FT	HELIx	208 214
FT	HELIx	217 221
FT	TURN	222 223
FT	STRAND	229 229
FT	HELIx	233 243
FT	TURN	244 244
FT	HELIx	247 249
FT	TURN	250 250
FT	TURN	253 254

FT	STRAND	256	263
PT	HELIX	274	276
Query Match			
Best Local Similarity 100.0%; Score 6106; DB 1; Length 1170;			
Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	MDSCITWAMALLSGFFFPASSYNLDVRGARSPPRARHRGRLQYQNGVYGA	60
DB	1	MDSCITWAMALLSGFFFPASSYNLDVRGARSPPRARHRGRLQYQNGVYGA	60
QY	61	PEEGNSTGLYQCQSGTGHCLEPTLRGSNYSKYLGMTLATPTGSLACDPSRTCD	120
DB	61	PEEGNSTGLYQCQSGTGHCLEPTLRGSNYSKYLGMTLATPTGSLACDPSRTCD	120
QY	121	QNTYLSGLCYLFRONLQGPMLQGRPGQECIKGNVDFELFDGSMSLQDPEFOKILDPMK	180
DB	121	QNTYLSGLCYLFRONLQGPMLQGRPGQECIKGNVDFELFDGSMSLQDPEFOKILDPMK	180
QY	181	DVMKLTSTSYCPAAVQSTSYKTEFSDYKAKDPALLKHYKMLLTTPGAINV	240
DB	181	DVMKLTSTSYCPAAVQSTSYKTEFSDYKAKDPALLKHYKMLLTTPGAINV	240
QY	241	DVMKLTSTSYCPAAVQSTSYKTEFSDYKAKDPALLKHYKMLLTTPGAINV	240
DB	241	DVMKLTSTSYCPAAVQSTSYKTEFSDYKAKDPALLKHYKMLLTTPGAINV	240
QY	301	KFASKPASEFVKILDTPEKLDLFTLOKIVIEIGTSKODLTSFMELSSGSIADLSR	360
DB	301	KFASKPASEFVKILDTPEKLDLFTLOKIVIEIGTSKODLTSFMELSSGSIADLSR	360
QY	361	GHAVVGAKDWMAGGFLDKLDDDTFIGNBPLTPRYAGYLGTTWLPSSROKTSIL	420
DB	361	GHAVVGAKDWMAGGFLDKLDDDTFIGNBPLTPRYAGYLGTTWLPSSROKTSIL	420
QY	421	ASGARPYOMGRVILFOBPOGGGSHMSOVTHGTOIGSFEGELGVUNVDGCEFTLLI	480
DB	421	ASGARPYOMGRVILFOBPOGGGSHMSOVTHGTOIGSFEGELGVUNVDGCEFTLLI	480
QY	481	GAPLFYGBRGGRVFIYORROLGFEEVESELOQDPGYLGRFEALITATLDINGDLVVA	540
DB	481	GAPLFYGBRGGRVFIYORROLGFEEVESELOQDPGYLGRFEALITATLDINGDLVVA	540
QY	541	VGAPEEBOGAVYTFNGRHGSLSPQSORIEGQVLSGIQWFRSHGVADLEGDLAAVA	600
DB	541	VGAPEEBOGAVYTFNGRHGSLSPQSORIEGQVLSGIQWFRSHGVADLEGDLAAVA	600
QY	601	VGAESOMIVLSRPVVDWTLMSFSPARIPVHEVSCYSTSKMKKEGVNTTCPOIKSLY	660
DB	601	VGAESOMIVLSRPVVDWTLMSFSPARIPVHEVSCYSTSKMKKEGVNTTCPOIKSLY	660
QY	661	POFOGRVLANLTYTLQDGHRTTRRGLFPQGRHELRRIAVTTSMSCTDFSHFPVCOD	720
DB	661	POFOGRVLANLTYTLQDGHRTTRRGLFPQGRHELRRIAVTTSMSCTDFSHFPVCOD	720
QY	721	LISPIVNSLNSLWEEBGPDDQRAQKDIPIILAPSLHSETWELPERKCEGDKKCBAN	780
DB	721	LISPIVNSLNSLWEEBGPDDQRAQKDIPIILAPSLHSETWELPERKCEGDKKCBAN	780
QY	781	LIVSFPSPARSLRLTAFAASLVELSLNLEBDAAVWOLDLHFPGLSFRKYMELKPSQ	840
DB	781	LIVSFPSPARSLRLTAFAASLVELSLNLEBDAAVWOLDLHFPGLSFRKYMELKPSQ	840
QY	841	IPVSCCELPEESRLSLRALSQVSSPIPKAGSHVALQMMFNTLVSSSGDSVELLANTC	900
DB	841	IPVSCCELPEESRLSLRALSQVSSPIPKAGSHVALQMMFNTLVSSSGDSVELLANTC	900
QY	901	NNBBDLLEDSNATITIPILPINILIDQENSTYVSTPGPKTIHQYKMYQVRIOPS	960
DB	901	NNBBDLLEDSNATITIPILPINILIDQENSTYVSTPGPKTIHQYKMYQVRIOPS	960
QY	961	IHDHNIPTLEAVGVGPPESEGPITHQMSVQMEPPVPCHYEDLERLPDAAPCPLGALFR	1020

DB	961	IHDHNIPTLEAVGVGPPESEGPITHQMSVQMEPPVPCHYEDLERLPDAAPCPLGALFR	1020
QY	1021	CPVVFROEILVQVIGTLELVEIEIASMSFISLSSISFNSSKPHLYGNSLAQVYMK	1080
DB	1021	CPVVFROEILVQVIGTLELVEIEIASMSFISLSSISFNSSKPHLYGNSLAQVYMK	1080
QY	1081	VDVYVEKMLLYLVLSGIGLILLLIFIVLYXYGFPFRNLKEMWEGRGVNGIPADS	1140
DB	1081	VDVYVEKMLLYLVLSGIGLILLLIFIVLYXYGFPFRNLKEMWEGRGVNGIPADS	1140
QY	1141	EQLASGEAGDPCGLKPLHEKDSGSGGKD	1170
DB	1141	EQLASGEAGDPCGLKPLHEKDSGSGGKD	1170
RESULT 2			
ID	096HB1	PRELIMINARY;	PRT; 1086 AA.
AC	096HB1		
DT	01-DEC-2001 (TREMBLrel. 19, Created)		
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)		
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)		
DE	ITGL protein.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Lymph;		
RX	MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Ditachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Stapleton M.J., Uedl T.B., Toshitsuki S., Carninci P., Prange C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,		
RA	Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,		
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fatey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,		
RA	Whitting M., Madan A., Young A.C., Shevchenko Y., Boultard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,		
RA	Kryzhanek M.I., Skalski U., Smalhe D.B., Schermer A., Schein J.E.,		
RA	Jones S.J., Marra M.A.,		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences."		
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Lymph;		
RA	Strausberg R.,		
RL	Submitted (May-2001) to the EMBL/GenBank/DBJ databases.		
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).		
CC	-1- SIMILARITY: Belongs to the integrin alpha chain family.		
DR	EMBL; BC008777; AH08777.1; -		
DR	HSSP; P20701; IDQO.		
DR	GO; GO:0016021; C:Integral to membrane; IEA.		
DR	GO; GO:0008305; C:Integrin complex; IEA.		
DR	GO; GO:0005515; F:protein binding; IEA.		
DR	GO; GO:0007160; P:cell-matrix adhesion; IEA.		
DR	GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.		
DR	InterPro; IPR000413; Integrin_alpha.		
DR	InterPro; IPR002035; VWP_A.		
DR	Pfam; PF00357; Integrin_alpha_1.		
DR	Pfam; PF00092; VWA_1.		
DR	PRINTS; PR01185; INTEGRINA.		
DR	PRINTS; PR00453; VWPADOMAIN.		
DR	SMART; SM00191; Int_alpha_5.		
DR	SMART; SM00327; VWA_1.		

DR PROSITE; PS00242; INTEGRIN\_ALPHA; 1.  
 DR PROSITE; PS50234; VWFA; 1.  
 KW Cell adhesion; Integrin; Transmembrane.  
 SQ SEQUENCE 1086 AA; 119223 MW; F6F2546E8C632F9 CRC64;

Query Match 91.5%; Score 5585; DB 2; Length 1086;  
 Best Local Similarity 92.7%; Pred. No. 0;  
 Matches 1085; Conservative 0; Mismatches 1; Indels 84; Gaps 2;

```

QY 1 MKDCITVMAMALLSGFFFPAPASSYNLDVVGARSFSPRRGRHGVVLDVGVGVYGA 60
DB 1 MKDCITVMAMALLSGFFFPAPASSYNLDVVGARSFSPRRGRHGVVLDVGVGVYGA 60
QY PGEENSTSLYQCSQGTGHCPTVLRGNSNTSKYLGMTLADPTDGTSLACDPGLSRCTD 120
DB PGEENSTSLYQCSQGTGHCPTVLRGNSNTSKYLGMTLADPTDGTSLACDPGLSRCTD 120
QY 61 PGEENSTSLYQCSQGTGHCPTVLRGNSNTSKYLGMTLADPTDGTSLACDPGLSRCTD 109
DB 61 PGEENSTSLYQCSQGTGHCPTVLRGNSNTSKYLGMTLADPTDGTSLACDPGLSRCTD 109
QY 121 QNTYLSGLCYLFRONLQGPMLQGRPGQECIKGNVDLVFLFDGSMSLQPDFQKILDFMK 180
DB 121 QNTYLSGLCYLFRONLQGPMLQGRPGQECIKGNVDLVFLFDGSMSLQPDFQKILDFMK 180
QY 110 ----- 109
DB 110 ----- 109
QY 181 DVMKLSTNTSYQFAVQFSTSYKTEPDSYVYKGRDPALLKHYKMLLTNTGALNVY 240
DB 181 DVMKLSTNTSYQFAVQFSTSYKTEPDSYVYKGRDPALLKHYKMLLTNTGALNVY 240
QY 110 -----FAVQFSTSYKTEPDSYVYKGRDPALLKHYKMLLTNTGALNVY 157
DB 110 -----FAVQFSTSYKTEPDSYVYKGRDPALLKHYKMLLTNTGALNVY 157
QY 241 ATEVFRRELGARPDATKVLIIITDGEATDSGNIDAKDIIRYIIGIGHFQTKESQETLH 300
DB 241 ATEVFRRELGARPDATKVLIIITDGEATDSGNIDAKDIIRYIIGIGHFQTKESQETLH 300
QY 158 ATEVFRRELGARPDATKVLIIITDGEATDSGNIDAKDIIRYIIGIGHFQTKESQETLH 217
DB 158 ATEVFRRELGARPDATKVLIIITDGEATDSGNIDAKDIIRYIIGIGHFQTKESQETLH 217
QY 301 KFAKSPASEPVKIIDTFEKLKDLFTELOKTIYIEIGTSKODLTSPFMELSSSGISADLSR 360
DB 301 KFAKSPASEPVKIIDTFEKLKDLFTELOKTIYIEIGTSKODLTSPFMELSSSGISADLSR 360
QY 218 KFAKSPASEPVKIIDTFEKLKDLFTELOKTIYIEIGTSKODLTSPFMELSSSGISADLSR 277
DB 218 KFAKSPASEPVKIIDTFEKLKDLFTELOKTIYIEIGTSKODLTSPFMELSSSGISADLSR 277
QY 361 GHAVVAGAVGADMGAGFLDLKADLODDTFIGNBPLTEPVKAGYGYTWTMLPSRQKTSLL 420
DB 361 GHAVVAGAVGADMGAGFLDLKADLODDTFIGNBPLTEPVKAGYGYTWTMLPSRQKTSLL 420
QY 278 GHAVVAGAVGADMGAGFLDLKADLODDTFIGNBPLTEPVKAGYGYTWTMLPSRQKTSLL 337
DB 278 GHAVVAGAVGADMGAGFLDLKADLODDTFIGNBPLTEPVKAGYGYTWTMLPSRQKTSLL 337
QY 421 ASGAPRYOHMGRVLLFOEPQGGGHWISQVQTHIGTQIGYFGGELCGVVDVDDGETELLII 480
DB 421 ASGAPRYOHMGRVLLFOEPQGGGHWISQVQTHIGTQIGYFGGELCGVVDVDDGETELLII 480
QY 338 ASGAPRYOHMGRVLLFOEPQGGGHWISQVQTHIGTQIGYFGGELCGVVDVDDGETELLII 397
DB 338 ASGAPRYOHMGRVLLFOEPQGGGHWISQVQTHIGTQIGYFGGELCGVVDVDDGETELLII 397
QY 481 GAPLFGYGEORGARVFIYQRRLGFEVEVELQSDPGVPLGRFGEAITALTIDINGDLVDVA 540
DB 481 GAPLFGYGEORGARVFIYQRRLGFEVEVELQSDPGVPLGRFGEAITALTIDINGDLVDVA 540
QY 398 GAPLFGYGEORGARVFIYQRRLGFEVEVELQSDPGVPLGRFGEAITALTIDINGDLVDVA 457
DB 398 GAPLFGYGEORGARVFIYQRRLGFEVEVELQSDPGVPLGRFGEAITALTIDINGDLVDVA 457
QY 541 VGAPLEBEGGAVYIFNGRHGGLSPQPSORIETGVLSGIQWFGRSIHGVKDEBGLADVA 600
DB 541 VGAPLEBEGGAVYIFNGRHGGLSPQPSORIETGVLSGIQWFGRSIHGVKDEBGLADVA 600
QY 458 VGAPLEBEGGAVYIFNGRHGGLSPQPSORIETGVLSGIQWFGRSIHGVKDEBGLADVA 517
DB 458 VGAPLEBEGGAVYIFNGRHGGLSPQPSORIETGVLSGIQWFGRSIHGVKDEBGLADVA 517
QY 601 VGASQMTVLSRPPVDWVTLMSPFPAIPIVHEVCSYSTSNKMGKGNITICFOIKSLY 660
DB 601 VGASQMTVLSRPPVDWVTLMSPFPAIPIVHEVCSYSTSNKMGKGNITICFOIKSLY 660
QY 518 VGASQMTVLSRPPVDWVTLMSPFPAIPIVHEVCSYSTSNKMGKGNITICFOIKSLY 577
DB 518 VGASQMTVLSRPPVDWVTLMSPFPAIPIVHEVCSYSTSNKMGKGNITICFOIKSLY 577
QY 661 POFQGRVLANITTYTLQDLGHRTRRRGLFPGGRHBLRNNIAVTTSMSCDTFSFHPVVCQD 720
DB 661 POFQGRVLANITTYTLQDLGHRTRRRGLFPGGRHBLRNNIAVTTSMSCDTFSFHPVVCQD 720
QY 578 POFQGRVLANITTYTLQDLGHRTRRRGLFPGGRHBLRNNIAVTTSMSCDTFSFHPVVCQD 637
DB 578 POFQGRVLANITTYTLQDLGHRTRRRGLFPGGRHBLRNNIAVTTSMSCDTFSFHPVVCQD 637
QY 721 LISPIVNSLNTSMEESTPRDQAGDIPILRSLHSETWEIPEFRKNGEDKKCAN 780
DB 721 LISPIVNSLNTSMEESTPRDQAGDIPILRSLHSETWEIPEFRKNGEDKKCAN 780
QY 638 LISPIVNSLNTSMEESTPRDQAGDIPILRSLHSETWEIPEFRKNGEDKKCAN 696
DB 638 LISPIVNSLNTSMEESTPRDQAGDIPILRSLHSETWEIPEFRKNGEDKKCAN 696
QY 781 LRVFSPPARSALRLTAPASLSVELSLNLEDAVWOLDLHFPPLGKFRKVMKPKPSQ 840
DB 781 LRVFSPPARSALRLTAPASLSVELSLNLEDAVWOLDLHFPPLGKFRKVMKPKPSQ 840
QY 697 LRVFSPPARSALRLTAPASLSVELSLNLEDAVWOLDLHFPPLGKFRKVMKPKPSQ 756
DB 697 LRVFSPPARSALRLTAPASLSVELSLNLEDAVWOLDLHFPPLGKFRKVMKPKPSQ 756
QY 841 IPVSCBELPEERSRLISRALSCNVSPPIFKAGSHVALQMMFNTLVNMSGDSVELHANVC 900
DB 841 IPVSCBELPEERSRLISRALSCNVSPPIFKAGSHVALQMMFNTLVNMSGDSVELHANVC 900
QY 757 IPVSCBELPEERSRLISRALSCNVSPPIFKAGSHVALQMMFNTLVNMSGDSVELHANVC 816
DB 757 IPVSCBELPEERSRLISRALSCNVSPPIFKAGSHVALQMMFNTLVNMSGDSVELHANVC 816
QY 901 NNEDSDLLIEDNSATTTIPIILYPINLIDQDSDSTLYVFTFKGPKIHQVKMYQVRIOPS 960
DB 901 NNEDSDLLIEDNSATTTIPIILYPINLIDQDSDSTLYVFTFKGPKIHQVKMYQVRIOPS 960
QY 817 NNEDSDLLIEDNSATTTIPIILYPINLIDQDSDSTLYVFTFKGPKIHQVKMYQVRIOPS 876
DB 817 NNEDSDLLIEDNSATTTIPIILYPINLIDQDSDSTLYVFTFKGPKIHQVKMYQVRIOPS 876

```

```

QY 961 IHDHNIPTLEAVVGVPPPESEGPITTHQMSVQMEPPVPCHEYDELERLDPDAEPCLPGALFR 1020
DB 877 IHDHNIPTLEAVVGVPPPESEGPITTHQMSVQMEPPVPCHEYDELERLDPDAEPCLPGALFR 936
QY 1021 CPVVFROEIIIVQYITGTELVEGBIASSMFLCSGLSTFNSSGHFHLVGSNASTLAQVVMK 1080
DB 937 CPVVFROEIIIVQYITGTELVEGBIASSMFLCSGLSTFNSSGHFHLVGSNASTLAQVVMK 936
QY 1081 VDVVYERKQMLLYLVLSGIGLTLTLTLFIYLYVYVGFPRKRLKEKMEAGRGVPNGIPAEDE 1140
DB 997 VDVVYERKQMLLYLVLSGIGLTLTLTLFIYLYVYVGFPRKRLKEKMEAGRGVPNGIPAEDE 1056
QY 1141 EQLASGQEADPGCLXPLHEKDESEGGGKD 1170
DB 1057 EQLASGQEADPGCLXPLHEKDESEGGGKD 1086

RESULT 3
ITAL_BOVIN STANDARD; PRT; 1165 AA.
AC P61625;
DT 05-JUN-2004 (Rel. 44, Created)
DT 05-JUN-2004 (Rel. 44, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Integrin alpha-L precursor (Leukocyte adhesion glycoprotein LFA-1 alpha chain) (LFA-1A) (Leukocyte function associated molecule 1, alpha chain) (CD11a).
DE Name=ITGAL;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA PubMed=14697514; DOI=10.1016/j.gene.2003.09.043;
RX Felt T., Zecchion L., Baise B., Desmecht D.;
RT "The bovine (Bos taurus) CD11a-encoding cDNA: molecular cloning, characterisation and comparison with the human and murine glycoproteins."
RT Gene 325:97-101(2004).
RL CC -1- FUNCTION: Integrin alpha-L/beta-2 is a receptor for ICAM1, ICAM2, ICAM3 and ICAM4. It is involved in a variety of immune phenomena including leukocyte-endothelial cell interaction, cytotoxic T-cell mediated killing, and antibody dependent killing by granulocytes and monocytes (By similarity).
CC -1- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-L associates with beta-2 (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.
CC -1- SIMILARITY: Belongs to the integrin alpha chain family.
CC -1- SIMILARITY: Contains 7 FG-GAP repeats.
CC -1- SIMILARITY: Contains 1 VWFA domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ebi.ac.uk/announcements or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; AY267467; AB94035.1; -
DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.
DR PROSITE; PS50234; VWFA; 1.
KW Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor; Repeat; Signal; Transmembrane.
FT CHAIN 1 23 Potential.
FT DOMAIN 24 1165 Integrin alpha-L.
FT TRANSMEM 1085 1105 Extracellular (Potential).
FT DOMAIN 1106 1165 Cytoplasmic (Potential).

```

```

FT REPEAT 40 88 FG-GAP 1.
FT REPEAT 89 146 FG-GAP 2.
FT DOMAIN 153 324 VMPA.
FT REPEAT 347 397 FG-GAP 3.
FT REPEAT 398 452 FG-GAP 4.
FT REPEAT 454 513 FG-GAP 5.
FT REPEAT 515 572 FG-GAP 6.
FT REPEAT 575 627 FG-GAP 7.
FT CA_BIND 465 473 Potential.
FT CA_BIND 527 535 Potential.
FT CA_BIND 587 595 Potential.
FT SITE 1111 1115 GFFKR motif.
FT DISULFID 71 78 By similarity.
FT DISULFID 108 126 By similarity.
FT DISULFID 650 704 By similarity.
FT DISULFID 768 774 By similarity.
FT DISULFID 842 858 By similarity.
FT DISULFID 994 1009 By similarity.
FT DISULFID 1017 1048 By similarity.
FT CARBOHYD 33 33 N-linked (GlcNAc...) (potential).
FT CARBOHYD 86 86 N-linked (GlcNAc...) (potential).
FT CARBOHYD 185 185 N-linked (GlcNAc...) (potential).
FT CARBOHYD 646 646 N-linked (GlcNAc...) (potential).
FT CARBOHYD 667 667 N-linked (GlcNAc...) (potential).
FT CARBOHYD 723 723 N-linked (GlcNAc...) (potential).
FT CARBOHYD 859 859 N-linked (GlcNAc...) (potential).
FT CARBOHYD 894 894 N-linked (GlcNAc...) (potential).
FT CARBOHYD 929 929 N-linked (GlcNAc...) (potential).
FT CARBOHYD 1056 1056 N-linked (GlcNAc...) (potential).
FT CARBOHYD 1067 1067 N-linked (GlcNAc...) (potential).
SQ SEQUENCE 1165 AA; 128725 MW; DAEB3A3F1E1463CB CRC64;

```

Query Match 76.3%; Score 4657.5; DB 1; Length 1165;  
 Best Local Similarity 77.3%; Pred. No. 1.7e-297;  
 Matches 901; Conservative 98; Mismatches 164; Indels 3; Gaps 3;

```

QY 3 DSCITVMMALISGFFFPASSVYLTVRGASRSPSPAPRGVTVGVNGVTVGAPG 62
DB 2 NSCIIVLRI-LISGPFVFPAMSYNLDVHVNQNSFPLAGRHFGVTVGVNGVTVGAPG 60
QY 63 EGNSTGSLYOCOSGTGHCIPVTLRGSNYSKYLGWTLATDPTDGSILACDPLSRTCCON 122
DB 61 EGNMGNLYOCQCPETGDCIPVTL-SSNTSKYLGLWTLATDPTDGLACDPLSRTCCON 119
QY 123 TYLSGLCYLFRONTQGMLOGRPGFQECIKGNVDLVFLFDGSMSLQDPDFOKIILDFMKDV 182
DB 120 TYLSGLCYLHBNLHGPVLOGHGPGYQECIKGNVDLVFLFDGSMSLQDPDFOKIILDFMKDV 179
QY 183 MKKLSNTSYQPAAPVQSTSYKTEFPSPDYVVRKDDALLKAYKMLLTNTFGAINVAT 242
DB 180 MKKLSNTSYQPAAPVQSTSYKTEFPSPDYVVRKDDALLKAYKMLLTNTFGAINVAT 239
QY 243 EYFRELGRAPDATVLIITITGSEATDSGNDAADIIIRYIIIGIKHFKOTRESORTLKF 302
DB 240 EYFRELGRAPDATVLIITITGSEATDSGNDAADIIIRYIIIGIKHFKOTRESORTLKF 299
QY 303 ASKPASFEVKILDTFEKLKDLTELQKKIYVIEGTSKODLTSFNNELSSSGISADLSRGH 362
DB 300 ASKPASFEVKILDTFEKLKDLTELQKKIYVIEGTSKODLTSFNNELSSSGISADLSRGH 359
QY 363 AVYGVAVKADWAGSLDKADLQDPTFGNEPLTEBVAAGYIGYVTVMLPSKQKTSLSLA 422
DB 360 GYVGVAVKADWAGSLDKADLQDPTFGNEPLTEBVAAGYIGYVTVMLPSKQKTSLSLA 419
QY 423 GAPRYOHGKRVLLFQPKRGKGSMSIQIETDQISYSYGGELCGVDVDRDGETELLILAA 482
DB 420 GAPRYOHGKRVLLFQPKRGKGSMSIQIETDQISYSYGGELCGVDVDRDGETELLILAA 479
QY 483 PLFYGEORGGRVFIYORRQLGFEVSELOQDGYPLGRRFGAITALTJINDGVLDAVVG 542
DB 480 PLFYGEORGGRVFIYORRQLGFEVSELOQDGYPLGRRFGAITALTJINDGVLDAVVG 539
QY 543 APLBEOGAVYIFNGHGGSLSPQSRIGTQVLSGIQFGRSHGVKDLBGDLADVAVG 602

```

```

DB 540 APLBEOGAVYIFNGHGGSLSPQSRIGTQVLSGIQFGRSHGVKDLBGDLADVAVG 599
QY 603 AESQWIVLSRPVDMVMTLMSFSPAELPVHEVECSYSTSNKMGKGVNTTICFOIKSLYPQ 662
DB 600 AESQWIVLSRPVDMVMTLMSFSPAELPVHEVECSYSTSNKMGKGVNTTICFOIKSLIST 659
QY 663 FQGRVAVNLTYTLQDGRTRRGLFPGGRHLELRNIAVTTSMGCTDSSFFPVCVDOLI 722
DB 660 FQGRVAVNLTYTLQDGRTRRGLFPGGRHLELRNIAVTTSMGCTDSSFFPVCVDOLI 719
QY 723 SPINVLNFSMBEGRPRDOAOQKDPILRLPSLSSETWEIPKCKGCDKCEANLR 782
DB 720 SPINVLNFSMBEGRPRDOAOQKDPILRLPSLSSETWEIPKCKGCDKCEANLR 779
QY 783 VSPFARSRALRLTAFASLYELSLSNLEBDAYVVOULHPPGLSFRKEMLKPHSQIP 842
DB 780 VSPFARSRALRLTAFASLYELSLSNLEBDAYVVOULHPPGLSFRKEMLKPHSQIP 839
QY 843 VSCBELPESRSLSPALSCNVSPIPKAGSHVALQMFNTLVNSMGDSVELHANTCN 902
DB 840 VSCBELPESRSLSPALSCNVSPIPKAGSHVALQMFNTLVNSMGDSVELHANTCN 899
QY 903 EDSULLENSATTTIPIIYPIINILIOQEDSTLYVSFTPKGPKTHOVKMTQVRIOPSIH 962
DB 900 EDSULLENSATTTIPIIYPIINILIOQEDSTLYVSFTPKGPKTHOVKMTQVRIOPSIH 959
QY 963 DHNIPTLEAVVGPDPSPSEGITTHQMSVOMEPVPVCHYEDLERLPDAAPCLPGALFPCP 1022
DB 960 DHNIPTLEAVVGPDPSPSEGITTHQMSVOMEPVPVCHYEDLERLPDAAPCLPGALFPCP 1018
QY 1023 VVFEQELIVQYITGLBELVGBIEASMSFSLCSLSISFNSSGHFHLXGNSALQAVMKVD 1082
DB 1019 VVFEQELIVQYITGLBELVGBIEASMSFSLCSLSISFNSSGHFHLXGNSALQAVMKVD 1078
QY 1083 VVFEQELIVQYITGLBELVGBIEASMSFSLCSLSISFNSSGHFHLXGNSALQAVMKVD 1142
DB 1079 VVFEQELIVQYITGLBELVGBIEASMSFSLCSLSISFNSSGHFHLXGNSALQAVMKVD 1138
QY 1143 LASQGEAGDPGCLKPLHEKDSRSGCG 1168
DB 1139 LASQGEAGDPGCLKPLHEKDSRSGCG 1164

```

RESULT 4  
 OCTYB8 PRELIMINARY; PRT; 1166 AA.  
 ID OCTYB8  
 AC OCTYB8  
 DT 05-JUL-2004 (TrEMBLrel. 27, last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, last annotation update)  
 DE Lymphocyte function-associated antigen 1 alpha subunit CD1A.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Kuminantia; Pecora; Bovidae;  
 OC Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN  
 RP SEQUENCE FROM N. A.  
 RA Dileepan T., Thumthik P., Kannan M.S., Maheswaran S.K.;  
 RL Submitted (SEP-2003) to the EMBL/Genbank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
 CC -1- SIMILARITY: Belongs to the integrin alpha chain family.  
 DR EMBL: AY382558; AAC90015.1; -.  
 DR GO: GO:0016021; C:integral to membrane; IEA.  
 DR GO: GO:0008305; C:protein complex; IEA.  
 DR GO: GO:0005515; F:protein binding; IEA.  
 DR GO: GO:0007160; P:cell-matrix adhesion; IEA.  
 DR GO: GO:0007229; P:integrin-mediated signaling pathway; IEA.  
 DR InterPro: IPR000413; Integrin\_alpha.  
 DR Pfam: PF01819; FG-GAP; 3\_.  
 DR Pfam: PF00357; Integrin\_alpha; 1.



DR Pfam; PF00092; VWA; 1.  
 DR PRINTS; PR01185; INTEGRINA.  
 DR PRINTS; PR00453; VWFADOMAIN.  
 DR SMART; SM00191; Int\_alpha; 5.  
 DR SMART; SM00327; VWA; 1.  
 DR PROSITE; PS00242; INTEGRIN\_ALPHA; 1.  
 DR PROSITE; PS50234; VWFA; 1.  
 KW Cell adhesion; Integrin; Transmembrane.  
 SQ SEQUENCE 1166 AA; 128723 MW; 78BD8AFBA896C9DF CRC64;

Query Match 74.9%; Score 4571.5; DB 2; Length 1166;  
 Best Local Similarity 75.9%; Pred. No. 8e-292;  
 Matches 886; Conservative 103; Mismatches 176; Indels 3; Gaps 3;

QY 1 MKDCITVMAALLSGFFFAFASYNLDVNGARSPRAGRHGGRVNLQVNGVYGA 60  
 DB 1 MKDCITVLRLLSGPFVFAFASYNLDVNVQSPFPLGRHGVYLVQGVGVVGA 59  
 QY PGEKSTSLYOCOSGTGHCPLVTLRGSNYTSKYLGMTLATDPTDGLIACDPGLSRPCD 120  
 DB PSEKSNMGNLYOCQEPETGDCPLPVL-SSNYTSKYLGMTLATDPTSDNLACDPGLSRPCD 118  
 QY 121 QNTYLSGLCYLFRONTLOGPMLQGRPFQECIKGNVDVLFDFGSMISLPDEFOKILDFMK 180  
 DB QNTYLSGLCYLIHEVLRGPVLQGHGPGYQECIKGNVDVLFDFGSMISLPDEFOKILDFMK 178  
 QY 119 QNTYLSGLCYLFRONTLOGPMLQGRPFQECIKGNVDVLFDFGSMISLPDEFOKILDFMK 180  
 DB 119 QNTYLSGLCYLFRONTLOGPMLQGRPFQECIKGNVDVLFDFGSMISLPDEFOKILDFMK 180  
 QY 181 DVMKLSTSYOFAVOSTSYKTEPDSYVYKRDPAALLKHYKMTLLNTTGTATNYV 240  
 DB 181 DVMKLSTSYOFAVOSTSYKTEPDSYVYKRDPAALLKHYKMTLLNTTGTATNYV 240  
 QY 179 DVMKLSTSYOFAVOSTSYKTEPDSYVYKRDPAALLKHYKMTLLNTTGTATNYV 238  
 DB 179 DVMKLSTSYOFAVOSTSYKTEPDSYVYKRDPAALLKHYKMTLLNTTGTATNYV 238  
 QY 241 ATEVFRBELGARPDATKYLIIITDGEATDSGNIDAADIIYIIIGIGHPQTKESQETLH 300  
 DB 241 ATEVFRBELGARPDATKYLIIITDGEATDSGNIDAADIIYIIIGIGHPQTKESQETLH 300  
 QY 239 AKVFRPRLGARPDATKYLIIITDGEATDSGNIDAADIIYIIIGIGHPQTKESQETLH 298  
 DB 239 AKVFRPRLGARPDATKYLIIITDGEATDSGNIDAADIIYIIIGIGHPQTKESQETLH 298  
 QY 301 KFAKSPASEFYKIIDTFEKLKDLFTELQKIIYVIGTSKODLTSPFMELSSSGISADLSR 360  
 DB 299 OFASKPVEEFYKIIDTFEKLKDLFTELQKIIYVIGTSKODLTSPFMELSSSGISADLSR 358  
 QY 361 GHAVANGAGADMAGGFLDRLADLDDFFIGNEPLITPEVRAGYLGTYTWTMLPSRQKSTLL 420  
 DB 359 GHAVANGAGADMAGGFLDRLADLDDFFIGNEPLITPEVRAGYLGTYTWTMLPSRQKSTLL 418  
 QY 421 ASGARPYOMGRVLLFQEPQSGHMSQVOTIHGTQIGSYFGGELCGVVDODGSETLLI 480  
 DB 419 ATGAPKYOHVGRVLLFQEPQSGHMSQVOTIHGTQIGSYFGGELCGVVDODGSETLLI 478  
 QY 481 GAPPFYEGORGRVFIYGRDQLGFESEVSELOQDPGYLGRFGELATLTALTDINGDLVDVA 540  
 DB 479 AAPLYFGORGRVFIYGRDQLGFESEVSELOQDPGYLGRFGELATLTALTDINGDLVDVA 538  
 QY 541 VGAPLEBEGAVYIFNGRHGGLSPQSORIEGTQVLSGIQWGRGSHGVKDLLEGDLADVA 600  
 DB 539 VGAPLEBEGAVYIFNGRHGGLSPQSORIEGTQVLSGIQWGRGSHGVKDLLEGDLADVA 598  
 QY 601 VGASQOMIVLSRPVVDWTLMSPFAPRIPVHEVCSYSTSNKMGVNTITCFQIKSLY 660  
 DB 599 VGABEQVIVLSRPVVDIITSVSBPAIIPVHEVCSYSTSNKMGVNTITCFQIKSLY 658  
 QY 661 POFQRLVANTTYTLQDLGHRTRRRGLPPGGRHLELRNIAVTSNCTDPSFHPFVQVD 720  
 DB 659 STFOGHVANTTYTLQDLGHRTRRRGLPPGGRHLELRNIAVTSNCTDPSFHPFVQVD 718  
 QY 721 LISPLINVLNLSWEEBETPRDQAGKODIPPIILPSLSHSETWEIPEFKNGCEDKCCAN 780  
 DB 719 LISPLINVLNLSWEEBETPRDQAGKODIPPIILPSLSHSETWEIPEFKNGCEDKCCAN 778  
 QY 781 LRVSPSPRSALRTTAASISVELSLNLEDAVWVOLDLHPPGSLFRKYEMLKPSQ 840  
 DB 779 LKLAFSDMRSKILRLTPSASISVRLTLNLTADAADVAVVYTLSPFGSLFRKYEMLKPSH 838  
 QY 841 IPVSCCELPEBSRLSLRALSCNVSSPIFKAGSHVALQWMTLVNNSWGDSEVELHANTYC 900  
 DB 839 VPVCEELPEBAVSHRALSNCVSSPIFGEDSMVDIQWMTLVNNSWGDSEVELHANTYC 898

QY 901 NNEDSDLENNASATTIPIILYINILIQOEDSTLYVSPFKPKITHQVAMYOVRIOPS 960  
 DB 899 NNEDSDLENNASATTIPIILYINILIQOEDSTLYVSPFKPKITHQVAMYOVRIOPS 958  
 QY 961 IHDNIPFLBAVGVPOPPSEGPITTHQMSVQVMEPPVCHYEDLERLDDAEPCLPGALFR 1020  
 DB 959 NYD-NMPFLBAVGVPOPPSEGPITTHQMSVQVMEPPVCHYEDLERLDDAEPCLPGALFR 1017  
 QY 1021 CPVVFROEILVOYITGIELVGEIBASMSBLSLSISFNSSKHFLYGSNASIAQVYMK 1080  
 DB 1018 CPVVFROEILVOYITGIELVGEIBASMSBLSLSISFNSSKHFLYGSNASIAQVYMK 1077  
 QY 1081 VDVYKEMKLYLYLSGIGLILLLIFITYLYKVPFRKRLKEMKAGRGVPGIPAEBS 1140  
 DB 1078 VDVYKEMKLYLYLSGIGLILLLIFITYLYKVPFRKRLKEMKAGRGVPGIPAEBS 1137  
 QY 1141 EQLASQEGADPGCLKPLHEKDSRSGG 1168  
 DB 1138 GQPELBKCKDPSCLERPLNHTDDBSGG 1165

RESULT 5  
 Q9WTV4 PRELIMINARY; PRT; 1161 AA.  
 AC Q9WTV4;  
 DT 01-NOV-1999 (TREMURel. 12, Created)  
 DT 01-NOV-1999 (TREMURel. 12, Last sequence update)  
 DT 01-MAR-2004 (TREMURel. 26, Last annotation update)  
 DE Integrin alpha L.  
 GN Name=Itgal;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DKA/2J; TISSUE=spleen;  
 RA Ma R.2., Teuscher C.;  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).  
 CC -1- SIMILARITY: Belongs to the integrin alpha chain family.  
 DR EMBL; AF065902; AAD25885.1; -.  
 DR HSSP; P20701; IDGO.  
 DR MED; MG1.96506; Itgal.  
 DR GO; GO:0005615; C:extracellular space; TAS.  
 DR GO; GO:0016021; C:integral to membrane; TAS.  
 DR InterPro; IPR000413; Integrin\_alpha.  
 DR InterPro; IPR02035; VWF\_A.  
 DR Pfam; PF001839; FG-GAP; 1.  
 DR Pfam; PF00357; Integrin\_alpha; 1.  
 DR Pfam; PF00092; VWA; 1.  
 DR PRINTS; PR01185; INTEGRINA.  
 DR PRINTS; PR00453; VWFADOMAIN.  
 DR SMART; SM00191; Int\_alpha; 5.  
 DR SMART; SM00327; VWA; 1.  
 DR PROSITE; PS00242; INTEGRIN\_ALPHA; 1.  
 DR PROSITE; PS50234; VWFA; 1.  
 KW Cell adhesion; Integrin; Transmembrane.  
 SQ SEQUENCE 1161 AA; 128240 MW; 86B102F7B209E431 CRC64;

Query Match 71.5%; Score 4365.5; DB 2; Length 1161;  
 Best Local Similarity 72.6%; Pred. No. 3e-278;  
 Matches 839; Conservative 124; Mismatches 185; Indels 7; Gaps 6;

QY 13 LLSGFFFAFASYNLDVNGARSPRAGRHGGRVNLQVNGVYGAPEGKSTGSLYQ 72  
 DB 11 LLSGLOFAPAKMSYNLDTRPTQSTL-AQAGRHCYQVLQLEDGVVGAPEGKSTGSLYH 69  
 QY 73 COSGTGHCPLVTLRGSNYTSKYLGMTLATDPTDGSIIACDPGLSRPCDONTYLSGLCYLP 132  
 DB 70 CRTSSEFCQVDSVLSHGNSHTSKYLGMTLATDAAGSIIACDPGLSRPCDONTYLSGLCYLP 129

```

QY 133 RQNLQPMLOGRPGFOECIKGNVDFLPDGSMSLOPDEFOKILDPMDKVMKKLSNTSYQ 192
DB 130 PSLGSGPMLQNRPAVOECMKGVDFLPDGSQSLDRKDFEKLLEPMKVMKKLSNTSYQ 189
QY 193 PAAVOFSTSYKTEBDFSDYVR-KDPDALLKHVKHMLLTNTFGAINVATEVFEELGA 251
DB 190 PAAVOFSTDCRTEBFLDYVQKNKPDVLLGSVQPMFLTNTFPAINVVAHVFEBSGA 249
QY 252 RPDATKVLIIITDGEATDGSNIDAAKDIRIYIIGKHFQYKESQETLHKPASKPASEFV 311
DB 250 RPDATKVLIIITDGEATDGSNIDAAKDIRIYIIGKHFVSVOXKTLHIFASEBVEEFV 309
QY 312 KIUDPEFKKDLFTELQKKIYIIEGTSKODLTSFNMELSSSGISADLSRGAHVGAVGAK 371
DB 310 KIUDPEFKKDLFTELQKKIYIIEGTSKODLTSFNMELSSSGISADLSRGAHVGAVGAK 369
QY 372 DWAGGFLLDKADLODDFTIGNEPLTPEVAGYLGTYTWLPFRQKTSILASGAPRYOHMG 431
DB 370 DWAGGFLLDKADLODDFTIGNEPLTPEVAGYLGTYTWLPFRQKTSILASGAPRYOHMG 429
QY 432 RVLLFOEPQGGHWSQVQTIHGTOIGSYFGGELCGVVDVQDGETELLIGAPLFYGEORG 491
DB 430 RVLLFOEPQGGHWSQVQTIHGTOIGSYFGGELCGVVDVQDGETELLIGAPLFYGEORG 489
QY 432 GRVFTYORRQLGFEVSELOQDPGYPLGRFGRAITALTINDGAVDVAVGAHFAEGAV 551
DB 430 GRVFTYORRQLGFEVSELOQDPGYPLGRFGRAITALTINDGAVDVAVGAHFAEGAV 549
QY 552 YIFNGRHGSLPQSPORIEGTQVLSGIOMFGSHIGVNDLEBDGLADVAGASQOMVLS 611
DB 550 YIFNGRHGSLPQSPORIEGTQVLSGIOMFGSHIGVNDLEBDGLADVAGASQOMVLS 609
QY 612 SRPVDVMTVLSFSPBAEIPVHEVECSYSTSNMKEGVNTTCFOIKSLYPOFQRLVANT 671
DB 610 SRPVDVMTVLSFSPBAEIPVHEVECSYSTSNMKEGVNTTCFOIKSLYPOFQRLVANT 669
QY 672 TYTLODGHRTTRRGFLPFGGRHKLKRNIAVTTSMGCTDPSFHPVPCVVDLSPINVSINF 731
DB 670 TYTLODGHRTTRRGFLPFGGRHKLKRNIAVTTSMGCTDPSFHPVPCVVDLSPINVSINF 729
QY 732 SLMBEGTPRDOAOKDIPILRPSLHSETWEIPFEKNGCGDKCEANTLRSVPASRSR 791
DB 730 SLMBEGTPRDOAOKDIPILRPSLHSETWEIPFEKNGCGDKCEANTLRSVPASRSR 786
QY 792 ALRLTAPASLSVELSLNLEBDAYVVDLHPPGSLSPFKVEMLKPHSQIPVSCBELPEB 851
DB 787 ALRLTAPASLSVELSLNLEBDAYVVDLHPPGSLSPFKVEMLKPHSQIPVSCBELPEB 846
QY 852 SLLSRALSCNVSSPFRAGHSAVALQAMNTLVNNGSGDVSRLANVTNNEDSLLBDN 911
DB 847 SLLSRALSCNVSSPFRAGHSAVALQAMNTLVNNGSGDVSRLANVTNNEDSLLBDN 906
QY 912 SATTIIPILYPIINIILODEDSTLVSPFKGPKLHOVMYQVRIOPSIHDPNPTLEA 971
DB 907 SATTIIPILYPIINIILODEDSTLVSPFKGPKLHOVMYQVRIOPSIHDPNPTLEA 966
QY 972 VVGVPQPSSEGPITQWVSQVMEPVPVCHYEDLER-LPDAEPCLGALFRCPVPEREITL 1030
DB 967 VVGVPQPSSEGPITQWVSQVMEPVPVCHYEDLER-LPDAEPCLGALFRCPVPEREITL 1026
QY 1031 VOYITGLBVGIEKASSMFSGLSSISFNSKHFHLYGSNANSLAQVVMKVDVVEKQML 1090
DB 1027 VOYITGLBVGIEKASSMFSGLSSISFNSKHFHLYGSNANSLAQVVMKVDVVEKQML 1086
QY 1091 VYVYLSGIGGLLLIIFVLVYKVPFKRNLEKKNKBAAGRVNGPAPEDSEOLA-SGORA 1149
DB 1087 VYVYLSGIGGLLLIIFVLVYKVPFKRNLEKKNKBAAGRVNGPAPEDSEOLA-SGORA 1146
QY 1150 GDPGLKPLHKEKDE 1164
DB 1147 KDMGCLBPLREBDDK 1161

```

```

RESULT 6
Q9R200 PRELIMINARY; PRT; 1160 AA.
ID Q9R200
AC Q9R200;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Integrin alpha L.
GN Integrin;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spleen;
RA Ma R.Z., Teuscher C.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
-1- SIMILARITY: Belongs to the Integrin alpha chain family.
DR EMBL; AF065901; AAD25884.1; -.
DR HSSP; P20701; IDQO.
DR MGJ; MGJ:96606; Itgal.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR00413; Integrin_alpha.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF01839; Fg-GAP; 1.
DR Pfam; PF00357; Integrin_alpha; 1.
DR Pfam; PF00092; VWA; 1.
DR PRINTS; PR01185; INTEGRINA.
DR SMART; SM00453; VWFADOMAIN.
DR SMART; SM00191; Int_alpha; 5.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.
DR PROSITE; PS00234; VWF_A; 1.
KW Cell adhesion; Integrin; Transmembrane.
SQ SEQUENCE 1160 AA; 128127 MW; A33C531B139F1PAD CRC64;

Query Match 71.4%; Score 4361; DB 2; Length 1160;
Best Local Similarity 72.6%; Pred. No. 5,8e-278;
Matches 838; Conservative 123; Mismatches 187; Indels 6; Gaps 5;
QY 13 LLSGFFPAPASSYNLDVGRASFSPPRAGHFGYRLVQVNGYLVGAPGEGNSTGSLYQ 72
DB 11 LLLGLQFAKAMSYNLDTRPQSF-L-ADAGHFGYQVLIIDGVVVGAPGEGDNTGGLYH 69
QY 73 QSGTGHLPTVTLGNSNTSKYLGMTLATDPTDGSIIACDPGLSRTCPQNTYLSGLCYLF 132
DB 70 CRTSEFCQPVSLHSGNSHTSKYLGMTLATDPAKGSLLACDGLSRTCPQNTYLSGLCYLF 129
QY 133 RQNLQPMLOGRPGFOECIKGNVDFLPDGSMSLOPDEFOKILDPMDKVMKKLSNTSYQ 192
DB 130 PSLGSGPMLQNRPAVOECMKGVDFLPDGSQSLDRKDFEKLLEPMKVMKKLSNTSYQ 189
QY 193 PAAVOFSTSYKTEBDFSDYVR-KDPDALLKHVKHMLLTNTFGAINVATEVFEELGA 251
DB 190 PAAVOFSTDCRTEBFLDYVQKNKPDVLLGSVQPMFLTNTFPAINVVAHVFEBSGA 249
QY 252 RPDATKVLIIITDGEATDGSNIDAAKDIRIYIIGKHFQYKESQETLHKPASKPASEFV 311
DB 250 RPDATKVLIIITDGEATDGSNIDAAKDIRIYIIGKHFVSVOXKTLHIFASEBVEEFV 309
QY 312 KIUDPEFKKDLFTELQKKIYIIEGTSKODLTSFNMELSSSGISADLSRGAHVGAVGAK 371
DB 310 KIUDPEFKKDLFTELQKKIYIIEGTSKODLTSFNMELSSSGISADLSRGAHVGAVGAK 369
QY 372 DWAGGFLLDKADLODDFTIGNEPLTPEVAGYLGTYTWLPFRQKTSILASGAPRYOHMG 431
DB 370 DWAGGFLLDKADLODDFTIGNEPLTPEVAGYLGTYTWLPFRQKTSILASGAPRYOHMG 429
QY 432 RVLLFOEPQGGHWSQVQTIHGTOIGSYFGGELCGVVDVQDGETELLIGAPLFYGEORG 491

```

```

Db 430 QVLLFQADAEAGRMNQTKIEGTQIGSYFGGELSCVDDLDQGEAEILLIGALFFEGEORG 489
Qy 492 GRVFIYORROLGFEEVSELSQDPPGYLARGFEGALITATIDINDGDLVDAVAGAPLEBOGAV 551
Db 490 GRVFIYORROLGFEEVSELSQDPPGYLARGFEGALITATIDINDGDLVDAVAGAPLEBOGAV 549
Qy 552 YIFNGRHGGLSPQSPQSRIEQTQVLSGIQMPGKSIHGVDLEBGDLADVAAGASQMIYLS 611
Db 550 YIFNGKPGGLSPQSPQSRIEQTQVLSGIQMPGKSIHGVDLEBGDLADVAAGAPLEBOGAV 609
Qy 612 SRPVDMVTLMSFSPFAEIPVHEVECSYSTSKMEGNNITTCFQIKSLYPPQGGULVANTL 671
Db 610 SRPVDMVTLMSFSPFAEIPVHEVECSYSTSKMEGNNITTCFQIKSLYPPQGGULVANTL 669
Qy 672 TYTTLQDGHRTRRRRLFPFGGRHELRNIAVTTSMCTFSFHFAPVCVODLSPINVSINF 731
Db 670 TYTTLQDGHRTRRRRLFPFGGRHELRNIAVTTSMCTFSFHFAPVCVODLSPINVSINF 729
Qy 732 SLMBEETPPDQRAQKDIPIILRPSLHSEWEIPEKXNCGEDKCKCEANLAVSFPASR 791
Db 730 SLMBEETPPDQRAQKDIPIILRPSLHSEWEIPEKXNCGEDKCKCEANLAVSFPASR 786
Qy 792 ALRLTAFASVSELSTLSEBDAYVVOULHPPRGLSPKXKEMCKPHSQIPVSCHELEEB 851
Db 787 PLRLMSASLAVEMWTLNSGSDAYWRDLDPRLGLSPKXKEMCKPHSQIPVSCHELEEB 846
Qy 852 SRLLSRALSCNVSPSIFPAGHSVALQMMFNTLVNMGSDVSELANVYCNNEEDSLBDN 911
Db 847 SSLTLTKLKNVSPSIFPAGHSVALQMMFNTLVNMGSDVSELANVYCNNEEDSLBDN 906
Qy 912 SATTTIPIIPIYINILIQOEDSTLYVSTTPKPKTHQVKNMYQVRIQPSIHDMNITPLEA 971
Db 907 SAATHIPIIPIYINILIQOEDSTLYVSTTPKPKTHQVKNMYQVRIQPSIHDMNITPLEA 966
Qy 972 VGVGPQPSSEGITQMSVQMPVPCYHDELEPDAEPCLPALRCPCVPRQETLV 1031
Db 967 LVGVPRPSEDLITITWVQDPLVTCSEDKRSSAEPCLPVQPCPIVFWELL 1026
Qy 1032 QVITGLLELVGEIEASMFSLCSLSISFNSSKHFHLYGSNASLQVWKNVYVVEKOMLY 1091
Db 1027 QVITGLLELVGEIEASMFSLCSLSISFNSSKHFHLYGSNASLQVWKNVYVVEKOMLY 1086
Qy 1092 LVTLSGIGGLLLLIPIVLYKVGFKKLNKKEWAGRGVNGIIPAEDEOLA-SGQFAG 1150
Db 1087 VYVLSGIGGLVLIPIVLYKVGFKKLNKKEWAGRGVNGIIPAEDEOLA-SGQFAG 1146
Qy 1151 DPGCLKPLHEKDE 1164
Db 1147 DMGCLLEPLESDDK 1160

```

```

RN [2]
RP SEQUENCE OF 24-42.
RX MEDLINE=65188276; PubMed=387182;
RA Springer T.A., Teplov D.B., Dreyer W.J.,
RT "Sequence homology of the LFA-1 and Mac-1 leukocyte adhesion
RL glycoproteins and unexpected relation to leukocyte interferon.";
Nature 314:540-542(1985).
CC -1- FUNCTION: Integrin alpha-L/beta-2 is a receptor for ICAM1, ICAM2,
CC ICAM3 and ICAM4. Is involved in a variety of immune phenomena
CC including leukocyte-endothelial cell interaction, cytotoxic T-cell
CC mediated killing, and antibody dependent killing by granulocytes
CC and monocytes. Mice expressing a null mutation of the alpha-L
CC subunit gene demonstrate impaired tumor rejection and impaired
CC leukocytes recruitment.
CC -1- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-L
CC associates with beta-2.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Leukocytes.
CC -1- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins
CC with I-domains do not undergo protease cleavage.
CC -1- SIMILARITY: Belongs to the integrin alpha chain family.
CC -1- SIMILARITY: Contains 7 FG-GAP repeats.
CC -1- SIMILARITY: Contains 1 VWFA domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M60778; AAA39426.1; -.
DR PIR; I56126; I56126.
DR HSSP; P20701; IDGQ.
DR MGD; MGI:96606; Itgal.
DR InterPro; IPR000413; Integrin_alpha.
DR InterPro; IPR02035; VWF_A.
DR Pfam; PF01839; FG-GAP; 2.
DR Pfam; PF00357; Integrin_alpha; 1.
DR Pfam; PF00092; VWFA; 1.
DR PRINTS; PRO1185; INTEGRINA.
DR SMART; SM00453; VWFADOMAIN.
DR SMART; SM00191; Int_alpha; 5.
DR SMART; SM00327; VWFA; 1.
DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.
DR PROSITE; PS50234; VWFA; 1.
KW Calcium; Cell adhesion; Direct protein sequencing; Glycoprotein;
KW Integrin; Magnesium; Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 23
FT CHAIN 24 1163
FT DOMAIN 24 1087
FT TRANSMEM 1088 1108
FT DOMAIN 1109 1163
FT REPEAT 89 146
FT REPEAT 39 325
FT DOMAIN 153 348
FT REPEAT 348 398
FT REPEAT 399 454
FT REPEAT 455 514
FT REPEAT 516 573
FT REPEAT 576 628
FT CA_BIND 466 474
FT CA_BIND 528 536
FT CA_BIND 588 596
FT SITE 1111 1115
FT DISULFID 70 77
FT DISULFID 108 126
FT DISULFID 147 199
FT DISULFID 651 705
FT DISULFID 767 773
FT DISULFID 840 856
FT DISULFID 993 1009

```

```
FT DISULFID 1017 1048 BY similarity.
FT CARBOHYD 86 86 N-linked (GlcNAc . . .) (potential)
FT CARBOHYD 185 185 N-linked (GlcNAc . . .) (potential)
FT CARBOHYD 270 270 N-linked (GlcNAc . . .) (potential)
FT CARBOHYD 270 270 N-linked (GlcNAc . . .) (potential)
FT CARBOHYD 444 444 N-linked (GlcNAc . . .) (potential)
FT CARBOHYD 668 668 N-linked (GlcNAc . . .) (potential)
FT CARBOHYD 696 696 N-linked (GlcNAc . . .) (potential)
FT CARBOHYD 724 724 N-linked (GlcNAc . . .) (potential)
FT CARBOHYD 728 728 N-linked (GlcNAc . . .) (potential)
FT CARBOHYD 776 776 N-linked (GlcNAc . . .) (potential)
FT CARBOHYD 857 857 N-linked (GlcNAc . . .) (potential)
FT CARBOHYD 880 880 N-linked (GlcNAc . . .) (potential)
FT CARBOHYD 890 890 N-linked (GlcNAc . . .) (potential)
FT CARBOHYD 899 899 N-linked (GlcNAc . . .) (potential)
FT CARBOHYD 927 927 N-linked (GlcNAc . . .) (potential)
FT CARBOHYD 1056 1056 N-linked (GlcNAc . . .) (potential)
SQ SEQUENCE 1163 AA; 128343 MW; A7A307848958232F CRC64;

Query Match
Best Local Similarity 71.1%; Score 4343.5; DB 1; Length 1163;
Matches 836; Conservative 123; Mismatches 182; Indels 7; Gaps 6;

13 LLSGFFPAASSYNDVVGARSFSPRAGRHFYGVAVGVNGVIVGAPGEGNSTGSLYQ 72
11 LLLGLQFLAKKASYNDLFRPQSGFL-AQAGRHFYGVAVGVNGVIVGAPGEGNSTGSLYH 69
73 CQSGTGHCLPVTLRSSNTSKYLGMTLATDPTDSSILACDPGLSRTCDONTYLSGLCYLF 132
70 CRTSEFPQCPVSLHSGNSHTSKYLGMTLATDAKGSLLACDPGLSRTCDONTYLSGLCYLF 129

133 RNLQGPMLQGRPGQECIKGNVDLVFLFDGNSISQPEFQKILDPMDVMKLSNTSYQ 192
130 PQLSGPMLQGNPAVQECIKGNVDLVFLFDGNSISQPEFQKILDPMDVMKLSNTSYQ 189
193 FAAYQFSTSYKTEPFPSDYKVR-KDPDALIKTKVKNLLTNFGAIVYVATEVFEETGA 251
190 FAAYQFSTDCRTEFFLDYVKNKRPDVLGSGVQMFLLTNFRALINVAHVFEETGA 249
252 RPDATKVLIIITDGATDSGNIDAAKIIIRYIIIGIKGFPQTKBSQETLHKFASKPASBFV 311
250 RPDATKVLIIITDGASDKGNISAAHDITRYIIIGIKGFVSQVQKTLHIFASBVEFEV 309
312 KILDTFEKLDLFTLQKIKYIESTSKODLTSFMWELSSSGISADLSKGAHVAVGAK 371
310 KILDTFEKLDLFTLQKIRIYAIESTNQDLTSFMWELSSSGISADLSKGAHVAVGAK 369
372 DWAGFLLDKADLQDPTFIGNBPLTPPEYRAGLYGTWYLPQRQTSLLASGAPRYQMG 431
370 DWAGFLLDKRDLQCATFVGGEPPLSDVARGSLGTLTVAMTSSRSRPLLAGAPRYQMG 429
432 RYLLFQEPQGGHWSQVOTIHGTQIGSYFGELGCVVDVODGETELLIGAPLPFYGEQRG 491
430 QYLLFQAPBAGGRMWTOKIEGTQIGSYFGELGCVVDVODGETELLIGAPLPFYGEQRG 489
492 GRVFIYQRRQLGFEVSEIQLGDPGPGPLRGFAGATLALTDINGDLVAVGAPLEEQAV 551
490 GRVFIYQRRQSLFEVSEIQLGDPGPGPLRGFAGATLALTDINDRLTDVAVGAPLEEQAV 549
552 YIFNGRHGGLSPQSORIEGTQVLSGIOWFGSHGVNDLBEQGLADVAVGASCOMITLS 611
550 YIFNGRHGGLSPQSORIQGAOVFPGRIRMGSHGVNDLBEQGLADVAVGASCOMITLS 609
612 SRPVVDWYTLMSFSPAEIPVHEVECSYSTSNKKEGVNITICFOIKSLIYPOFQSLVANT 671
610 SRPVVDWYTLMSFSPAEIPVHEVECSYSTSNKKEGVNITICFOIKSLIYPOFQSLVANT 669
672 TYTTLQDGHRTRRRLGPFGRHRLRNNTAVTSMGCTPSPFRPVCVDLSPINVSINF 731
670 STYTLQDGHRTRRRLGPFGRHRLRNNTAVTSMGCTPSPFRPVCVDLSPINVSINF 729
732 SLMBEGTTPRQDRAQKDIPIILRPSLSETWIEPFXKNGCGDKCEANLTVSFPASR 791
730 SLMBEGTTPRQDRAQKDIPIILRPSLSETWIEPFXKNGCGDKCEANLTVSFPASR 786
```

```
QY 792 ALRLTAPASLSVELSLNBERDAYWQDLAFPPGLSTRKYEMLKPHSQIPVSCHELPBE 851
DB PLRLMSSASLAVENTLNSGSDAYWRLDLPFPGSLFRKYEMLKPHSRMPEVSCHELTG 846
QY 852 SRLSRALSCNVSPFPAGSHVALQWMTLVNSWMDSVYELHANTVCNNEDSDLEBN 911
DB SSLTKITKCNVSPFPAGSHVALQWMTLVNSWMDSVYELHANTVCNNEDSDLEBN 906
QY 912 SATTIPIPLYPINILIDQDSTLYVSETPKGPRIHQVKMYOYRIOPSIDHNIPTLEA 971
DB SAATHIPIPLYPINILITKEQENSTLYISFTPGPKTQVQHYQYRIQSAVDHNPTEA 966
QY 972 VVGVPQPSSEPIRHQSVQWQEPFPCYEDLER-LPDAAPCIPGALFPCPVYFRQITL 1030
DB LVGVPQPSSEPIRHQSVQWQEPFPCYEDLER-LPDAAPCIPGALFPCPVYFRQITL 1026
QY 1031 VQVIGTLELVGEIEASWFSLSISISFNSKPFHLYGSNASIAQVMAKYDVVYERQML 1090
DB IQVIGTLELVGEIEASWFSLSISISFNSKPFHLYGSNASIAQVMAKYDVVYERQML 1086
QY 1091 YLYVLSGIGLILLLLPIYLYKVGFPKRNLIKEMAGRGVNGIPAEBSOLA-SQGEA 1149
DB HYYVLSGIGLILLLLPIYLYKVGFPKRNLIKEMAGRGVNGIPAEBSOLA-SQGEA 1146
QY 1150 GDPGCLKP 1157
DB 1147 KDMGCLBP 1154

RESULT 8
Q8HZV0 PRELIMINARY; PRT; 927 AA.
AC Q8HZV0;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Lymphocyte function-associated antigen 1 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovine; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Thumblak P., Kannan M.S., Maheswaran S.K.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the Integrin alpha chain family.
DR EMBL; AF440778; AAN63636.1; -.
DR HSSP; P20701; IDQO.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0008305; C:Integrin complex; IEA.
DR GO; GO:0005515; F:Protein binding; IEA.
DR GO; GO:0007160; F:Cell-matrix adhesion; IEA.
DR GO; GO:0007229; P:Integrin-mediated signaling pathway; IEA.
DR InterPro; IPR000413; Integrin_alpha.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF01839; FG-GAP; 2.
DR Pfam; PF00092; VWA; 1.
DR PRINTS; PR01185; INTEGRIN.
DR SMART; SM00191; Int_alpha; 4.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.
DR PROSITE; PS0234; VWF_A; 1.
KW Cell adhesion; Integrin; Transmembrane.
FT NON_TER 1
FT NON_TER 927
SQ SEQUENCE 927 AA; 102522 MW; 02E2CF09917081EC CRC64;

Query Match
Best Local Similarity 59.7%; Score 3644.5; DB 2; Length 927;
Matches 706; Conservative 84; Mismatches 134; Indels 1; Gaps 1;
```

```

QY 196 VQFSTSYKTEBDFSDYVVRKDPDALLKHVKHMLLTNTFGAINVATEVFEELGARDPA 255
D 4 VQFSTYFTEBTEFLDYIRKQDPDALLAGVKHMLLTNTFGAINVAKAVFPPDLGARDPA 63
QY 256 TKVTLITTDGATBSGNIDAAKDIIIRYIIGIKHFOYKESQETLHKFASKPSEFVKILD 315
D 64 TKVTLITTDGATBSGNIDAAKDIIIRYIIGIKHFOYKESQETLHKFASKPSEFVKILD 123
QY 316 TFEKLDLFTLQKKIYIEGTSKODLTSPMSELSSGISADLSRGHVAAGAKOMAG 375
D 124 TFEKLDLFTLQKKIYIEGTSKODLTSPMSELSSGISADLSRGHVAAGAKOMAG 183
QY 376 GFLLDKADLQDDTFIGNEPITPEVAGYLGTVTLTPSROKTSLLASGAPRYOHMGRVTL 435
D 184 GFLLDKADLQDDTFIGNEPITPEVAGYLGTVTLTPSROKTSLLASGAPRYOHMGRVTL 243
QY 436 FOEPOGGHMSQVOTIHGTQIGSYFGELCGVDVDQDETLLIIGAPLFGEOGRGVF 495
D 244 FOEPOGGHMSQVOTIHGTQIGSYFGELCGVDVDQDETLLIIGAPLFGEOGRGVF 303
QY 496 IYOROLGFEVSELOSDPGYPLGRFGAIALTDINDGLVDVAVGAPLEOGAVYIEN 555
D 304 IYOKIOLFQVSELOSTGTPLGRFGAIALTDINDGLVDVAVGAPLEOGAVYIEN 363
QY 556 GRHGLSPQSPQRIEGTQVLSGIQWFGRSIHGVNDLBDGLADAVAGAESQMIYLSRPV 615
D 364 GQGGGLSPRSPQRIEGTQVMSFGIQWFGRSIHGVNDLBDGLADAVAGAESQMIYLSRPV 423
QY 616 VDMYTLSPSPAEIPVHEVECSYSTSNMKEGVNTTIPQIKSLYPOGRVANLYTL 675
D 424 VDIYTLSPSPAEIPVHEVECSYSTSNMKEGVNTTIPQIKSLYPOGRVANLYTL 483
QY 676 QLDGRTERRGLPFGGRHELRNIAVTSMGCTDPSFHPVCYODLSPINVSINFSIME 735
D 484 QLDGRTERRGLPFGGRHELRNIAVTSMGCTDPSFHPVCYODLSPINVSINFSIME 543
QY 736 BEGTPRODQAKDIPILRPSLSEETWIEPPEKXCGEDKCEANLRYSPASSRALRT 795
D 544 BEGTPRODQAKDIPILRPSLSEETWIEPPEKXCGEDKCEANLRYSPASSRALRT 603
QY 796 TAPASLSELSLNEEDAVYVOLDLHPREGLSFRKVMLEKXSOIPVSCBLEPESRL 855
D 604 TAPASLSELSLNEEDAVYVOLDLHPREGLSFRKVMLEKXSOIPVSCBLEPESRL 663
QY 856 SRAISCNVSPPIFKAGHSVALOMMENTLVNSMGDSVLANVYNNNDSDLLDENATY 915
D 664 SRAISCNVSPPIFKAGHSVALOMMENTLVNSMGDSVLANVYNNNDSDLLDENATY 723
QY 916 IIPFLYINILIOQOEDSTLYVFTPKPKLHOVKMTQVRIOPSIDHNIPTLEAVGV 975
D 724 SIPWYPIINVLTQOENSTLYISFTPKSPRIHNVHAIQVRIQPSNDV-NMPPEALVRY 782
QY 976 POPSESEITQMSVQNEPVPCHYEDLERLDDAERCLPALFRCVAVFQOZILVOYIG 1035
D 783 PRVSEBGLITKMSIQMESPNCSPRNLESPEDESCESPFTEFRCPIDFQOZILVOYIG 842
QY 1036 TLEHVEIEMSMESLCSLSISFNSSKHFLXGMSLAQVMKNVYVEKMLYLYVL 1095
D 843 MVEHRTKASSMSLCSLSISFNSSKHFLXGMSLAQVMKNVYVEKMLYLYVL 902
QY 1096 SGIGLILLIFLIVLYKVGFFKEN 1120
D 903 SGIGLILLIFLIVLYKVGFFKEN 927

```

RESULT 9

Q6KAS4 PRELIMINARY; PRT, 1188 AA.

Q6KAS4  
AC Q6KAS4  
DT 05-JUL-2004 (TRENDEL. 27, Created)  
DT 05-JUL-2004 (TRENDEL. 27, Last sequence update)  
DT 05-JUL-2004 (TRENDEL. 27, Last annotation update)

```

DE MFLJ00114 protein (Fragment).
GN Name=MFLJ00114;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Suga Y., Kikuno R., Nakagawa T., Nagase T., Ohara O., Koga H.;
RT "Prediction of the Coding Sequences of Mouse Homologues of Flt Genes:
RT The Complete Nucleotide Sequences of 110 Mouse Flt-Homologous cDNAs
RT Identified by Screening of Terminal Sequences of cDNA Clones Randomly
RT Sampled from Size-Fractionated Libraries."
RL DNA Res. 11:167-180(2004).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).
CC -1- SIMILARITY: Belongs to the Integrin alpha chain family.
DR EMBL; AK131133; BAD21383.1; -.
DR HSSP; P17301; IAOX.
DR GO; GO:0009897; C:external side of plasma membrane; IDA.
DR GO; GO:0016021; C:integral to membrane; TMS.
DR InterPro; IPR000413; Integrin_alpha.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF00357; Integrin_alpha; 1.
DR Pfam; PF00092; VWA; 1.
DR PRINTS; PR01185; INTEGRINA.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00191; Int_alpha; 5.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS00242; INTEGRIN_ALPHA; UNKNOWN_1.
DR PROSITE; PS50234; VWFA; 1.
DR KEGG; Cell adhesion; Integrin; Transmembrane.
FT NON TER 1
SQ SEQUENCE 1188 AA; 131248 MW; BD93107BDB84178 CRC64;

Query Match 25.9%; Score 1583.5; DB 2; Length 1188;
Best Local Similarity 34.4%; Pred. No. 5,4e-95;
Matches 416; Conservative 213; Mismatches 467; Indels 115; Gaps 37;

QY 4 SCITVMAALLSGFFPAPASSYNLDVRGARSPPRAGNHPGRVYQVNG-VIYAPG 62
D 21 SC-TWIAFLILLG---FVSCLGFLNDAEKPTNHR--MDGAEFHSVLYQYDSSWVVGAPK 74
QY 63 E--GNSTGLYOQSGSTGHCPLVTLR-GSNYTSKYLGMTLATDPTGSLIACDPGSR 118
D 75 EIRATNIGGLYKCGHTTGCEPSISLOVPRPAVMSGLSLAATNPSWILLACGPYVHT 134
QY 119 CDQNTYLSGLCYL---FRONTLOQPMLOGRPFQECIKGNVDLVLPFDGSMISLPDEFQK 174
D 135 CRENIYLTGLCFLLSSFSKQSNFPQAQ-----QECPKQODIVFLIDSGSISSTDFEK 189
QY 175 ILDPMDKMKKLSTNSQVPAVQSPSTSYKTEPSPDVVRKDDALLKHVKHMLLTNTF 234
D 190 MLDPVKAVMSQLORPSTRFSLMOPSDYFRVHFTFNNFISTSSPLSLDSVROLRGYTYTA 249
QY 235 GAINVATEVFEELGARPATKVLITTDG-BATDSGNIDA-----ANDIIRYIIGIG 287
D 250 SAIKAVITLFTTQSGARKQATKVLITTDGKQGDNLSDSYIPIAAKASITIRYALIGV 309
QY 288 KHPQKESQETLHKFASKPSEFVKILDITPEKLDLFTLQKKIYIEGTSKODLTSPFM 347
D 310 KAFYNEHSKQELKAIKMSPEHVEYFVENFDALKDLENQKEXIPIAIGETPTSSSTFEL 369
QY 348 ELSSSGISADLSRGHVAAGAKDMAAGFLDKADLQDDTFIGNEPITPEVAGYLGTV 407
D 370 EMSQEGFSAVFTDGPVLAAGVSPSWSGAFILPSNMR-PTFINMSGENDMDAYAGYS 428
QY 408 VTMLPSROKTSLLASGAPRYOHMGRVTLFOEPOGGHMSQVOTIHGTQIGSYFGELCGV 467
D 429 -TALAFKGVHSLILGAPRQHTQKVIIF--TQESRHRKPKSEYRGVQIQTSGASLCSV 485
QY 468 DVDQDETLLIIGAPLFGEOGRGVFIYOROLG--FEEVSELOSDPGYPLGRFGAIAL 525
D 468 DVDQDETLLIIGAPLFGEOGRGVFIYOROLG--FEEVSELOSDPGYPLGRFGAIAL 525

```

```

Db DMDRSDTDLVLIGVPHYHTRGQGVSCWMPGVGRBMHCGTTLHGEGHPWRFGAL 545
Qy 526 TALTDINDGLVAVGAPLEQ--GAYIENG-RHGCLSPQSRIGTQVLSGIQMG 582
Db 546 TVLGVNDSDLADVAIGAPEGEEENGAVYIFHGASRODIAPSPSRIASQIPSIQYFG 605
Qy 533 RSHGVKOLEGDLVAVGASOMIVASRPVVMATLMSPPAIPVHEVCGSYSN 642
Db 606 QSLSGQDLTRDGLVAVGSKRVLLKRLPRLVPTVHTPRLVSRVFECCQYAP 665
Qy 643 KMKEGVNTTCFOIKSLVPOFGRLVNLTYTLQDGHTRRRGHPGGR-HELRLNIAY 701
Db 666 EGTLS-DATVCLIHESPTQGLDRLSTVTPDLADHRLSTRALFKTKRALTRVTL 724
Qy 702 TTNSCTDPSFHFVYVODLSPINVSINFSIMEEETPRDQAKDIPILRPSLSE 761
Db 725 GLMKCESEVKTLLPACVEDSVPTIRLNFSL--GVAPISL--QNLQPLW--AVDQ 776
Qy 762 TW---EIPFKNGGDKKCEANLRVSPARSRLRLTRFASLVELSLNLEDAVWQ 818
Db 777 TLTASLPEKXGADHICQDDLVSVPFGPPDLKTLVGSDELAVTVVNSDGEBSYGT 836
Qy 819 LDHPPGLSPFKV-----MLKPSQ-----IPVCELEPEERLSTRALSCNV 864
Db 837 VTLPVPLSTRVABGVFLAKEDQWQRGSHLMCDSTDRQGL-WSTSCSR 895
Qy 865 SPIFKAGSVALQWMENTLVNSWGSVELHANTCNNEDDLLENSATTI--IPILY 921
Db 896 HVIFRGSGMTFLVFDVSPKAEGLDRLLRLARVSENN--VGPCTPTFQLEPLVKY 951
Qy 922 PINILIQOEDSTLYVSF-TPKGPKIHQVKNYQVRIQPSIHDIHPIPL----- 969
Db 952 AVYTMISSHDPTFKLNFSTSEKETSVEHNFVN--NLGQRPVPSINFWPIELKG 1008
Qy 970 EAVVGVPPSPSGPITTHQMSVOMBP--FVPCHYDLERLTPAARPCVPGALFRCPVFR 1026
Db 1009 EAVVVMVMSHPNPITOCRRNRKARTOPDLTHQKSPVLDSDICLH--LRCD---- 1061
Qy 1027 QEILVQVIGTL-ELVGEIEASSMFS-----LCSSLSISFNSSKHPLVGSNASL 1074
Db 1062 ----IPSLGILDELFLIKGNLSFGMISQTLQKVLILSBAITFNTVSQGLPGQAFV 1117
Qy 1075 -AQVMKADVYERKMLYLYSGIGULLLITVLYKGFPRKMKKKMEARG--V 1131
Db 1118 RAQTKTIVEMKVNHPVPLVIGSSVGGILLALITAILIKGFFRGYKEMLEBANQFV 1177
Qy 1132 PNDIPADESQ 1142
Db 1178 SDGTPTPVAQ 1188

RESULT 10
ITAX_MOUSE STANDARD; PRT; 1169 AA.
AC Q9QNH4;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Integrin alpha-X precursor (leukocyte adhesion glycoprotein p150,95
alpha chain) (leukocyte adhesion receptor p150,95) (CD11c).
GN Name=Itgax;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=dendritic cell;
RA Huang X., Gorski K., Tong C., Rattis P.-M., Tseng S.-Y., Pardoll D.,
RA Tsuchiya H.;
RL Submitted (DEC-1999) to the EMBL/Genbank/DBD databases.
CC -!- FUNCTION: Integrin alpha-X/beta-2 is a receptor for fibrinogen. It

```

```

CC recognizes the sequence G-P-R in fibrinogen. It mediates cell-cell
CC interaction during inflammatory responses. It is especially
CC important in monocyte adhesion and chemotaxis (By similarity).
CC -!- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-X
CC associates with beta-2 (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins
CC with I-domains do not undergo protease cleavage.
CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
CC -!- SIMILARITY: Contains 1 FG-GAP repeats.
CC -!- SIMILARITY: Contains 1 VWFA domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL; AF211864; AAF23492.1; -.
CC DR HSSP; P20702; IN3Y.
CC DR MGD; MGI:96609; Itgax.
CC DR GO; GO:0009897; C:external side of plasma membrane; IDA.
CC DR InterPro; IPR000413; Integrin_alpha.
CC DR InterPro; IPR002035; VWF_A.
CC DR Pfam; PF01839; FG-GAP; 3.
CC DR Pfam; PF00357; Integrin_alpha; 1.
CC DR Pfam; PF00092; VWFA; 1.
CC DR PRINTS; PR01185; INTEGRINA.
CC DR PRINTS; PR00453; VWFADOMAIN.
CC DR SMART; SM00191; Int_alpha; 5.
CC DR SMART; SM00327; VWFA; 1.
CC DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.
CC DR PROSITE; PS0234; VWFA; 1.
CC KW Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
CC Repeat; Signal; Transmembrane.
CC FT SIGNAL 1 19
CC FT CHAIN 20 1169
CC FT DOMAIN 20 1166
CC FT TRANSMEM 1117 1137
CC FT DOMAIN 1138 1169
CC FT REPEAT 34 87
CC FT REPEAT 88 ?
CC FT DOMAIN 152 330
CC FT REPEAT ? 402
CC FT REPEAT 403 454
CC FT REPEAT 456 518
CC FT REPEAT 519 577
CC FT REPEAT 582 634
CC FT CA_BIND 467 475
CC FT CA_BIND 531 539
CC FT CA_BIND 594 602
CC FT STB 1140 1144
CC FT DISULFID 69 76
CC FT DISULFID 108 126
CC FT DISULFID 656 711
CC FT DISULFID 770 776
CC FT DISULFID 858 873
CC FT DISULFID 1007 1031
CC FT DISULFID 1036 1041
CC FT CARBOHYD 89
CC FT CARBOHYD 267
CC FT CARBOHYD 393 393
CC FT CARBOHYD 734 734
CC FT CARBOHYD 949
CC FT CARBOHYD 1059
CC FT CARBOHYD 1084
CC FT CARBOHYD 1084
CC FT SEQUENCE 1169 AA; 129150 MW; C616412033C219A6 CRC64;
CC Query Match 25.9%; Score 1582.5; DB 1; Length 1169;
CC Best Local Similarity 34.4%; Pred. No. 6,1e-95;
CC Matches 416; Conservative 214; Mismatches 466; Indels 115; Gaps 37;

```



```

Qy 4 SCITVMAALLSGFFFPASSYINLDVGARSFSPPARGRHFGYKVLQVANG-VIVGAPG 62
Db 2 SC-TWIAFLILLG---FVSCIGFNLDAEKLTTHFH--MDAGFGRHVLQYDSMWVYVGA 55
Qy 63 E---GNSTGSLYOCOSGTHCLPVTLR-GSNYTSKYLKMTLATPTDOSIACDPGLSRT 118
Db 56 EIKATNOIGLGYKCGYHNGCEPISLOVPPAVNLSISLAAATNPSMLACGPTVHT 115
Qy 119 CDONTYLSGLCYL-----FRONTLOQPMLOGRPGFOECIGKGVNDLVFLPFGSMLOPDEFOX 174
Db 116 CRENIYLTGLCFLLSSSKOSONFTAO-----QECPKODODIVFLIDSSGISSTDEK 170
Qy 175 ILDFMKDVKKLSNTSYQPAVQSTSYKTEPDFSDYVKRDPDALKHVHMLLTNTF 234
Db 171 MLDFKAVMSQLOPSTPSTFSLMFGSDYPRVHFTFNPFISTSSPLSLGVSQVLRQYTYTA 230
Qy 235 GAINVVAATEVREELGAPDPATKULITTDG-EATDSGNIDA-----AKOIRYITIG 287
Db 231 SAKHVITELFTTOSGARQADATKVLITTDGRKQDINSYDSVLPMAABAIIRYALGVG 290
Qy 288 KHPQKESQETLHKFASRPASEFVKILDTPEKLDLFTLOKTVIYIGTSKQDLTSPNM 347
Db 291 KAFTHNSKQELKAIASMPSHYVPSVNFADKDIENQLEKFIPIALGETPSSSTPEL 350
Qy 348 ELSSSGISADLSRGHAVVAVGAKDMAGFLDLKADODDTFIGNEPITPEVRAGYLGYT 407
Db 351 EMSQEGFAVFTPDGPVLGAVGFSWGSAGFLYPSNMK-PPIFNNSGEMEMRDADYIGYS 409
Qy 408 VTMPSRCKTSLASGARFYOMGRVLLFOEPQCGHMSOVOTIHGTQISYFGELCGV 467
Db 410 -TALAFMWGVHSLILGARPHOHTGKVIF--TOBSRHRPKSEVAGTGIGSFGSGLCSV 466
Qy 468 DVDQDETLELLIGAPLFYGEORGRVFIYQROLG--FEEVSELQGPYGLRFGBAI 525
Db 467 DMDRQSDVLVIGPHYHETRGQVSVCPMPGVGSMHCGTTLHGQGHMGRFGAL 526
Qy 526 TALVDINGDLVDAVAGAPLEBO--GAVYIFNG-RHGGLSPQSORIGTOVLSGIQWFG 582
Db 527 TVLDGVNDGLADVAIGAPEGENRGAVYIFHGASRQDIAPSPORIASQIPSLQVFG 586
Qy 583 RSHGVKDLBEGDLADVAVGASQMTVLSRPVDMVTLMSPAPLIVHEVCSYSTSN 642
Db 587 QSLSGGQDLTRDGLVDAVGSKGRVLLRTPRILVSPVTHFTPAEISRSVFCEQVAP 646
Qy 643 KMKGVNTTICFOKSLVPOFQGRVANTLTITOLDGRTRRGFPGR-HELBRNAY 701
Db 647 EQLTS-DATVCLIHESPKTQGLDKRSVTFTDLALDHGRLLSTRALFKETKRALTRVKT 705
Qy 702 TTSMSCDTPSFHFPVCVODLISPINVSINFSLMEEGTTPDORAQGDIPILRPSLSE 761
Db 706 GLNHGCSVKKLLPACVEDSVTPITLRINFSL---VGVPISL---QVLQML--AVDDQ 757
Qy 762 TW---EIPFEXOCEDKKCEANLKVSESPARSRALRLTAFASLSVELSLNLEDAVWQ 818
Db 758 TYFASLPEFKNCGADHICQDDLSVFFPDLKTLVVSDELKLVANDVSHDGEYSYGT 817
Qy 819 LIDLRFPPLSFRKVE---MLKPHSQ-----IPVSCBELPESRILSRALSCVNS 864
Db 818 VTLVPVGLSFRRAVAGVFLRKEDQOMQRGQSHLMLCDSTPDRQGL-WSTSCSR 876
Qy 865 SPIFKAGHVALQMFNTLVANSSWGDSEVELHANTCNNEEDSLLEDSNATIT---IPLY 921
Db 877 HVIFRGSGQMTFIVTFDVSPPKALIGDRLLRLARVSENN---VGPCTKTTFQLELPKY 932
Qy 922 PINLIQDQEDSTLYVSF-TPKGPKIHQVKMYQVRIQPSIHDNIPTL----- 969
Db 933 AVYTMISHSDQFTKXINLSTSEKETSVEHRFYVN---NLGQRDVPVSIINFVWIELKG 989
Qy 970 EAVVGVPPSPSEGLPTHQWSQMEP---PVPCHFDLERLRLDAAPCLPGALFRCPVFR 1026
Db 990 EAVTVMVSHPNPLTQCYRNRLKFTQDPLDLTHQKSPVLDCSIADCLH---LRCD--- 1042

```

```

Qy 1027 QEILVOVIGTL-ELVGEIEASNMFSS-----LCSSLSISFNSKHFHLVGNASL 1074
Db 1043 ----IPSLGILDELXIFIKGNLSFGWISQTLQKKVLLLSBAITFNSTSVSQLEGGQAF 1098
Qy 1075 -AQVMMVDVVEKQMLYLVVLSGIGLLLLLFITLVXVGFPRKRLXKEMGRG--V 1131
Db 1099 PAQKRTVLEMYKXNPPVLLVGVSSVGLLLAITLALVYRAGFPKQRYKMLEBANQFV 1158
Qy 1132 PNGIPARDSRQ 1142
Db 1159 SDGTPTPQVAD 1169

RESULT 11
ITAM HUMAN
ID ITAM HUMAN STANDARD; PRT; 1152 AA.
AC P11215;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Integrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor MO1) (Neutrophil adherence receptor).
GN Name=ITGAM; Synonym=CD11b, CR3A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88315033; PubMed=2457584;
RA Corbi A.L., Kishimoto T.K., Miller L.J., Springer T.A.;
RT "The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, CD11b) alpha subunit. Cloning, primary structure, and relation to the integrins, von Willebrand factor and factor B.";
RL J. Biol. Chem. 263:12403-12411 (1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88190151; PubMed=2833753;
RA Arnaout M.A., Remold-O'Donnell B., Pierce M.W., Harris P., Tenen D.G.;
RT "Molecular cloning of the alpha subunit of human and guinea pig leukocyte adhesion glycoprotein Mo1: chromosomal localization and homology to the alpha subunits of Integrins.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:2776-2780 (1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88257215; PubMed=2454931; DOI=10.1083/jcb.106.6.2153;
RA Arnaout M.A., Gupta S.K., Pierce M.W., Tenen D.G.;
RT "Amino acid sequence of the alpha subunit of human leukocyte adhesion receptor Mo1 (complement receptor type 3).";
RL J. Cell Biol. 106:2153-2158 (1988).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=93123748; PubMed=8419480;
RA Fleming J.C., Pahl H.U., Gonzalez D.A., Smith T.F., Tenen D.G.;
RT "Structural analysis of the CD11b gene and phylogenetic analysis of the alpha-integrin gene family demonstrate remarkable conservation of genomic organization and suggest early diversification during evolution.";
RL J. Immunol. 150:480-490 (1993).
RN [5]
RP SEQUENCE OF 9-1153 FROM N.A.
RX MEDLINE=89098893; PubMed=2563162;
RA Hickey D.D., Hickey M.J., Ozols J., Baker D.M., Back A.L., Roth G.J.;
RT "cDNA sequence for the alpha M subunit of the human neutrophil adherence receptor indicates homology to integrin alpha subunits.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:257-261 (1989).
RN [6]
RP SEQUENCE OF 1-9 FROM N.A.
RX MEDLINE=92073318; PubMed=1683702;
RA Shelley C.S., Arnaout M.A.;
RT "The promoter of the CD11b gene directs myeloid-specific and

```



RT developmentally regulated expression.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:10525-10529(1991).  
 RN [7]  
 RP SEQUENCE OF 1-9 FROM N.A.  
 RC TISSUE=Blood;  
 RX MEDLINE=92144986; PubMed=1346576;  
 RA Paul H.L., Rosemarin A.G., Tenen D.G.;  
 RT "Characterization of the myeloid-specific CD11b promoter.";  
 RL Blood 79:865-870(1992).  
 RN [8]  
 RP SEQUENCE OF 17-31.  
 RX MEDLINE=87076671; PubMed=3539202; DOI=10.1016/0167-4838(86)90037-3;  
 RA Pierce M.W., Remold-O'Donnell E., Todd R.F. III, Arnaout M.A.;  
 RT "N-terminal sequence of human leukocyte glycoprotein Mol: conservation  
 across species and homology to platelet IIb/IIIa.";  
 RL Biochim. Biophys. Acta 874:368-371(1986).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 148-331.  
 RX MEDLINE=95171458; PubMed=7667070; DOI=10.1016/0092-8674(95)90517-0;  
 RA Lee J.O., Rieu P., Arnaout M.A., Hittington R.;  
 RT "Crystal structure of the A domain from the alpha subunit of integrin  
 CR3 (CD11b/CD18).";  
 RL Cell 80:631-638(1995).  
 RN [10]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 148-334.  
 RX MEDLINE=96363671; PubMed=8747460; DOI=10.1016/S0969-2126(01)00271-4;  
 RA Lee J.O., Bankston L.A., Arnaout M.A., Hittington R.C.;  
 RT "Two conformations of the integrin A-domain (I-domain): a pathway for  
 activation?";  
 RL Structure 3:1333-1340(1995).  
 RN [11]  
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 148-337.  
 RX MEDLINE=96362595; PubMed=9687375; DOI=10.1016/S0969-2126(98)00093-8;  
 RA Baldwin E.T., Sawyer R.W., Bryant G.L., Jr., Curry K.A.,  
 RA Fairbanks M.B., Finzel B.C., Garlick R.L., Heinrichson R.L.,  
 RA Horton N.C., Kelley L.L., Milder A.M., Moon J.B., Mott J.E.,  
 RA Muchler V.T., Tomich C.S., Watempaugh K.D., Wiley V.H.;  
 RT "Cation binding to the integrin CD11b I domain and activation model  
 assessment.";  
 RL Structure 6:923-935(1998).  
 RN [12]  
 RP 3D-STRUCTURE MODELING OF 17-616.  
 RX MEDLINE=96226734; PubMed=9560195; DOI=10.1073/pnas.95.9.4870;  
 RA Owyg C., Springer T.A.;  
 RT "Experimental support for a beta-propeller domain in integrin alpha-  
 subunits and a calcium binding site on its lower surface.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:4870-4875(1998).  
 CC -1- FUNCTION: Integrin alpha-M/beta-2 is implicated in various  
 adhesive interactions of monocytes, macrophages and granulocytes  
 as well as in mediating the uptake of complement-coated particles.  
 CC It is identical with CR-3, the receptor for the IgG fragment of  
 the third complement component. It probably recognizes the R-G-D  
 peptide in C3b. Integrin alpha-M/beta-2 is also a receptor for  
 fibrinogen, factor X and ICAM1. It recognizes P1 and P2 peptides  
 of fibrinogen gamma chain.  
 CC -1- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-M  
 associates with beta-2.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- TISSUE SPECIFICITY: Predominantly expressed in monocytes and  
 granulocytes.  
 CC -1- DOMAIN: The integrin I-domain (insert) is a VWF-A domain. Integrins  
 with I-domains do not undergo protease cleavage.  
 CC -1- SIMILARITY: Belongs to the integrin alpha chain family.  
 CC -1- SIMILARITY: Contains 7 FG-GAP repeats.  
 CC -1- SIMILARITY: Contains 1 VWF-A domain.  
 CC -1- DATABASE: NAMB=PROV; NOTE=CD guide CD11b entry;  
 WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd11b.htm".  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL; J03925; AAA59544.1; -;  
 DR EMBL; M18044; AAA59491.1; -;  
 DR EMBL; J04145; AAA59903.1; -;  
 DR EMBL; S52227; AAB24821.1; -;  
 DR EMBL; S52152; AAB24821.1; JOINED.  
 DR EMBL; S52153; AAB24821.1; JOINED.  
 DR EMBL; S52154; AAB24821.1; JOINED.  
 DR EMBL; S52155; AAB24821.1; JOINED.  
 DR EMBL; S52157; AAB24821.1; JOINED.  
 DR EMBL; S52159; AAB24821.1; JOINED.  
 DR EMBL; S52161; AAB24821.1; JOINED.  
 DR EMBL; S52164; AAB24821.1; JOINED.  
 DR EMBL; S52165; AAB24821.1; JOINED.  
 DR EMBL; S52167; AAB24821.1; JOINED.  
 DR EMBL; S52169; AAB24821.1; JOINED.  
 DR EMBL; S52170; AAB24821.1; JOINED.  
 DR EMBL; S52173; AAB24821.1; JOINED.  
 DR EMBL; S52174; AAB24821.1; JOINED.  
 DR EMBL; S52180; AAB24821.1; JOINED.  
 DR EMBL; S52181; AAB24821.1; JOINED.  
 DR EMBL; S52184; AAB24821.1; JOINED.  
 DR EMBL; S52189; AAB24821.1; JOINED.  
 DR EMBL; S52191; AAB24821.1; JOINED.  
 DR EMBL; S52192; AAB24821.1; JOINED.  
 DR EMBL; S52203; AAB24821.1; JOINED.  
 DR EMBL; S52212; AAB24821.1; JOINED.  
 DR EMBL; S52213; AAB24821.1; JOINED.  
 DR EMBL; S52216; AAB24821.1; JOINED.  
 DR EMBL; S52219; AAB24821.1; JOINED.  
 DR EMBL; S52220; AAB24821.1; JOINED.  
 DR EMBL; S52221; AAB24821.1; JOINED.  
 DR EMBL; S52222; AAB24821.1; JOINED.  
 DR EMBL; S52226; AAB24821.1; JOINED.  
 DR EMBL; M76724; AAA58810.1; -;  
 DR EMBL; M84477; AAA51960.1; -;  
 DR PIR; A1108; Model1; @=17-1152.  
 DR PDB; 1A8X; Model1; @=17-1152.  
 DR PDB; 1BHO; X-ray; 1/2=-.  
 DR PDB; 1BHO; X-ray; 1/2=-.  
 DR PDB; 1IDN; X-ray; 1/2=-.  
 DR PDB; 1IDO; X-ray; @=140-331.  
 DR PDB; 1JLM; X-ray; @=143-334.  
 DR PDB; 1MIU; X-ray; A=137-331.  
 DR PDB; 1MF7; X-ray; A=144-337.  
 DR PDB; 1N9Z; X-ray; A=140-335.  
 DR PDB; 1N9Z; X-ray; A=144-345.  
 DR PDB; 1N9Z; X-ray; A=144-345.  
 DR Genew; HGNC:6149; ITGAM.  
 DR MIM; 120980; -;  
 DR GO; GO:0008305; C:integrin complex; TAS.  
 DR GO; GO:0007155; P:cell adhesion; TAS.  
 DR InterPro; IPR000413; Integrin\_alpha.  
 DR InterPro; IPR02035; VWF\_A.  
 DR Pfam; PF01839; FG-GAP; 3.  
 DR Pfam; PF00357; Integrin\_alpha; 1.  
 DR Pfam; PF00092; VWA; 1.  
 DR PRINTS; PR01185; INTEGRINA.  
 DR PRINTS; PR00453; VWFADOMAIN.  
 DR SMART; SM00191; Int\_alpha; 5.  
 DR SMART; SM00327; VWA; 1.  
 DR PROSITE; PS00242; INTEGRIN\_ALPHA; 1.  
 DR PROSITE; PS50234; VWF-A; 1.  
 DR 3D-structure; Calcium; Cell adhesion; Direct protein sequencing;  
 KW Glycoprotein; Integrin; Magnesium; Receptor; Repeat; Signal;  
 KW Transmembrane.  
 KW SIGNAL  
 FT CHAIN 17 1152 Integrin alpha-M.  
 FT  
 Query Match 25.6%; Score 1562.5; DB 1; Length 1152;  
 Best Local Similarity 34.3%; Pred. No. 1-2e-93;  
 Matches 408; Conservative 212; Mismatches 466; Indels 105; Gaps 37;

```

Qy 6 ITWAMALLSGFFFPAPASSYNLDVGRARSPPRAGHFGYRLQV--GNGVIVGABPE- 63
Db 6 LLLTALTLCHGF-----NLDTENAMTFQ--ENAGFGQSVYQLQSGSVVVGABPEI 54
Qy 64 --GNGSTGSLVYCCSGTGCHLPVTLR--GSNTYSKYLGMTLADPDIDGSLIADPGLSRCTCD 120
Db 55 VAAQORSLVYCCDYSYSCBEPILRLQVPEAVNMISLGLSLAATSPPLIACGPPVTHQCS 114
Qy 121 ONTYLSGLCYLFRONLQGPMLQGRPGPOECIKG-----NVDVLPFDGSMSLQDPDEFOKTL 176
Db 115 ENTIVKGLCFLPGSNLR-----QOPKFPPEALRGCPDSDIAFLIDSGSIIIPDPRMK 170
Qy 177 DFMADVKKLSTNTSYOFAAVOFTSYKTEPDSYVYKAKDPDALKYKMHLLTNTFEGA 236
Db 171 EFVSTVMEQLKSKSTLFSLMQYSEFRHFFKFEKQNNPNRSLVYKPTQLGLGTHATG 230
Qy 237 INVYATVFERELARPDATVLLIITDGE--ATDSGNIDAARD-----IIRYIIGIKH 289
Db 231 IRKVRRELFNTNGARKKAFKILVITDGEKFCDPLEGEDVIPEADREGVIRYVIGVDA 290
Qy 290 FQTESOETHKFPASKPASEFVKLIDPEKXKDLFTBLQKTYVIEGSKODLISFMNEL 349
Db 291 FRSEKSKRELNTTASKEPRDHFVQNNPEALKTTIQNQLREKIFALBEGYQSGSSSFEHEM 350
Qy 350 SSSGISADLSRGAHVAGAKDWAGFLDKADLDQDTPFIGNBPLTEPVAGYLGYYVT 409
Db 351 SQBFSAITNGPLSTVSGYDWAQGVF--LYTSKEXSTFINMTRVYSDMDADALGVAA 409
Qy 410 WLPRQKTSLLASGAPRYQHWGRVLLPEBPQGGHWSOVOTIHTQIGSYGSELGYDV 469
Db 410 -IILRNQVOSLVTDAPRYOHIGLVAMFR--ONTGMESNANVKGQIGAVGASISCSYDV 466
Qy 470 DODGETELLIGAPLEFGORGRVFI--YOROLGFEVEBELQDPGYPLRGFEAITA 527
Db 467 DSKNSTDLVILGAHYHTEQTRGGQVSVPLFRGARWCDAVLIGSQQPIGRGAALTV 526
Qy 528 LTTDINGDLVNAVAPLAE--QGAVYIFNGRHG--GLSPQSORIEGTQVLSGJOWFGRS 584
Db 527 LGDVNGDMLTVALGAPGEDNRGAVVLFHGTSGSGISPSHSQRIASGLSPRLQYRQGS 586
Qy 585 IHGKYDLEGDLAVVAGAESQMLVLSRPVYDNTLMSPPALIPVHEVCSYSTSKM 644
Db 587 LSGGDYLMDELVLVYGAQGHVLLRSQPLRVKALIMEPRRVARVFPFCNQV--KG 645
Qy 645 KEGVNITICFOI--RSIVPOF--QGRVLNVLTYTLQDGHRTRRGIFPGGRHELRNTAVT 702
Db 646 KEAGEVAVCLAVQKSTRDRLRBOQIQSVVITDLALDSGRPHSRVFNETKSTRQTVL 705
Qy 703 -TSMCTDPSFHPVVOVLISPINVSLFSLMEBEKTPRDQROQKXIDPIILRPSLHSE 761
Db 706 GLTGTCEKTLKQLNCTIEDPVSPIVLRNLSL--VGRPLS--AFGN-----LAPVLAED 755
Qy 762 TWEL-----PREKCCGEDKCCBANLVSPSPARSPALRLTLPASLSVELSLNIEBDAYW 816
Db 756 AQRFTLALFPEKKCCGNDNICODDLSITFSMSLDCLVGCPREPRNVTVVTRNGDEBSYR 815
Qy 817 VOJLHPPPGSLPRKVEML--KPHSQIPVSCBELLERSRLSRAL--SCNVSSPIFXA 870
Db 816 TOVFFPPLDLSTYKRVSTLONQORSQWRKACES--ASTVSGALXSTGSIHPIPE 873
Qy 871 GHSVALQMPENTLVNNSGDSVELEHANTCNNEBSDLLEDSATTI--IFILYFINILI 927
Db 874 NSEYTFNITPDVDSKASLGNTLLKANTSENN--MPRNKHTEFOLELFXKAVYVNV 929
Qy 928 QDQEDSTLYVSFFPKPKIKHQVKMYOVRLOPSJHDNIPTLEAVVGVPPQSGEPIHQ 987
Db 930 TSHGVSTKYLNFTASENSTRVMOHQYV--SNKGOSLIP--ISLVFLVPAVLTQVIMDR 985
Qy 988 WSVQMEPPV--PCHYEDLERLPDAAPCLPGALFRCPVY-----FRQ 1027
Db 986 PQTFFSENLSSTCHTK--ERLPSHSD--FLAELKRAPVNCSIAVCORIQCDIFFPFIQIE 1041

```

```

Qy 1028 EILVQVITGLTELVGEIRAS-SMFSLCSLSISFNSSKGFHLYSNLSL-AQVWAKDVVY 1085
Db 1042 EFNATLKNSFPMWYKXTSHNHLIIVSTABEILFNDSVFTLLIPQGAFAVRQETKVPFE 1101
Qy 1086 EKQMLYLYVLSGIGLLILLIILFVLYKQGFPRNLRKEKAEARGVNGRP 1136
Db 1102 VPMPLPVLSSVGGILLILLIITAAVLYKGLGFFRQYKDMWSEG-GPGABP 1151

RESULT 12
ITAX HUMAN
AC ITAX_HUMAN STANDARD; PRT; 1163 AA.
ID P20702; Q81VA6;
DT 01-FEB-1991 (Rel. 17, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Integrin alpha-X precursor (leukocyte adhesion glycoprotein p150, 95
GN Name=ITGAX; Synonyms=CD11c;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88166645; PubMed=3327687;
RA Corbi A.L., Miller L.J., O'Connor K., Larson R.S., Springer T.A.;
RT "cDNA cloning and complete primary structure of the alpha subunit of a
RL leukocyte adhesion glycoprotein, p150, 95."
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90153906; PubMed=2303426;
RA Corbi A.L., Garcia-Aguilar J., Springer T.A.;
RT "Genomic structure of an integrin alpha subunit, the leukocyte p150, 95
RL molecule."
RN [3]
RP ERRATUM.
RA Corbi A.L., Garcia-Aguilar J., Springer T.A.;
RL J. Biol. Chem. 265:2782-2788(1990).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RC TISSUE=Blood;
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stepieton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toehiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wooley D.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny K.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton B., Kettelman M., Madan A.C., Rodriguez Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Botterfield Y.S.N., Krzywinski M.I., Skalka U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 20-43.
RX MEDLINE=87167596; PubMed=3549901;
RA Miller L.J., Wiebe M., Springer T.A.;
RT "Purification and alpha subunit N-terminal sequences of human Mac-1
RL and p150, 95 leukocyte adhesion proteins."
RL J. Immunol. 158:2381-2383(1997).
CC 1- FUNCTION: Integrin alpha-X/beta-2 is a receptor for fibrinogen. It

```

CC	recognizes the sequence G-P-R in fibrinogen. It mediates cell-cell
CC	interaction during inflammatory responses. It is especially
CC	important in monocyte adhesion and chemotaxis.
CC	- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-X
CC	associates with beta-2.
CC	- SUBCELLULAR LOCATION: Type I membrane protein.
CC	- TISSUE SPECIFICITY: Predominantly expressed in monocytes and
CC	granulocytes.
CC	- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins
CC	with I-domains do not undergo protease cleavage.
CC	- SIMILARITY: Belongs to the integrin alpha chain family.
CC	- SIMILARITY: Contains 7 FG-GAP repeats.
CC	- SIMILARITY: Contains 1 VWFA domain.
CC	-1- DATABASE: NAME=PROV; NOTE=CD guide CD1c entry;
CC	WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd1c.htm".
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
CC	-----
DR	EMBL; M81695; AAA59180.1; -.
DR	EMBL; M29165; -; NOT ANNOTATED CDS.
DR	EMBL; M29487; AAA51620.1; ALT SEQ.
DR	EMBL; M29482; AAA51620.1; JOINED.
DR	EMBL; M29483; AAA51620.1; JOINED.
DR	EMBL; M29484; AAA51620.1; JOINED.
DR	EMBL; M29485; AAA51620.1; JOINED.
DR	EMBL; M29486; AAA51620.1; JOINED.
DR	EMBL; BC038237; AAH38237.1; -.
DR	PIR; A36584; RMHTIC.
DR	PDB; 1N3Y; X-ray; A=141-338.
DR	Genew; HGNC:6152; ITGAX.
DR	MIM; 151510; -.
DR	GO; GO:0008305; C:integrin complex; TAS.
DR	GO; GO:0004872; F:receptor activity; TAS.
DR	GO; GO:0007155; P:cell adhesion; TAS.
DR	GO; GO:0009887; P:organogenesis; TAS.
DR	InterPro; IPR000413; Integrin_alpha.
DR	InterPro; IPR002035; VWF_A.
DR	Pfam; PF01839; FG-GAP; 3.
DR	Pfam; PF00357; Integrin_alpha; 1.
DR	Pfam; PF00092; VWF_A; 1.
DR	PRINTS; PRO1185; INTEGRINA.
DR	PRINTS; PRO0453; VWFADOMAIN.
DR	SMART; SM00191; Int_alpha; 5.
DR	SMART; SM00327; VWF; 1.
DR	PROSITE; PS00242; INTEGRIN_ALPHA; 1.
DR	PROSITE; PS50234; VWFA; 1.
KW	3D-structure; Calcium; Cell adhesion; Direct protein sequencing;
KW	Glycoprotein; Integrin; Magnesium; Polymorphism; Receptor; Repeat;
KW	Signal; Transmembrane.
KW	SIGNAL 1 19
FT	CHAIN 20 1163 Integrin alpha-X.
FT	DOMAIN 20 1107 Extracellular (Potential).
FT	TRANSMEM 1108 1128 Potential.
FT	DOMAIN 1129 1163 Cytoplasmic (Potential).
FT	REPEAT 34 87 FG-GAP 1.
FT	REPEAT 88 ? FG-GAP 2.
FT	DOMAIN 165 351 VWFA.
FT	REPEAT ? 401 FG-GAP 3.
FT	REPEAT 402 453 FG-GAP 4.
FT	REPEAT 455 517 FG-GAP 5.
FT	REPEAT 518 576 FG-GAP 6.
FT	REPEAT 581 633 FG-GAP 7.
FT	CA_BIND 466 474 potential.
FT	CA_BIND 530 538 potential.
FT	CA_BIND 593 601 potential.
FT	SITE 1131 1135 GFPR motif.
FT	DISULFID 69 76 By similarity.

Query Match	Best Local Similarity	Score	DB 1	Length
Matches 421, Conservative 193, Mismatches 473, Indels 115, Gaps 40	35.0%	1526.5	DB 1	1163
12	ALLSGFFPAPASSVNLDPVGRARSFSPRAGRHHGYRLQVNGG-VIVGAPG---GNST	67		
6	AAALLFTLALNSLGFNDTELTLAFRDSAG--FGDSVVOVQANSMVYVGAQKITAANQT	63		
68	GSLYQOCOSGTCGLPVTIR-GSNTSKYLGMTLATDPDSSIIACDPGLSFTCDONTYLS	126		
64	GGLYQCGSTACGEPFGLQVPRPAVNMVSLGSLASTSPQGLACGPVHNECGSNMYLT	123		
127	GLCYLFRONLQGP--MLQGRP-GRQECIKGVNDLVPLFDGMSLQDPDEFQKILDFPMKDV	183		
124	GLCYLFRONLQGP--MLQGRP-GRQECIKGVNDLVPLFDGMSLQDPDEFQKILDFPMKDV	178		
184	KGLSNTSYQFAVQFSTSYKTEPDFSDVVKKDBDALLKHVGMMLLTNTFGAINVYATE	243		

```

Db 179 S Q F O R P S T Q S I M O F S N K F Q T H F T F E E P R T S N P L S L A S V H Q L G F T Y T A T A I O N V H R 238
Oy 244 V F R E B L G A R P A T K V L I I T D - - - - G E A T D S G N I - - - - D A A K D I R Y I I G I G K P Q T K E S 295
Db 239 L F H A S Y G A R R A T K I L I Y T D G K E G D S L D Y K D V I P M A D A - G I I R I A I G L A P O N E N S 297
Oy 296 Q E T I H K F A S K A S E F V K I L D T F E K L K D L F T E L O K K I Y I E G T S K O D L T S P M M E L S S G I S 355
Db 298 W K E I N D I A S K P S O E H I F V E D P D M K D I O N Q L K E K I P A I E G H E T T S S S F E L M A Q E F S 357
Oy 356 A D L S R G H A V G A N G A K M A G G F L D K A L O D D T F I G N E P L P E V A G I L T T V T M L B R Q 415
Db 358 A V F P D G P V L G A V G S F T W S G A F - L Y P P N M S P T F I M S O E N V M D M S T L G Y S - T E L A L M K 415
Oy 416 K T S L I A S G A P R Y O H N G R V L F O E P O G G G H W S O V T I H G N O I G S Y G E G E L C G V D V D O D E T 475
Db 416 G V O S I V L G A P R Y O H T K A V I F - T O V S R O M K M K A V T O T O I G S Y G A S L C S V D V D T D S T 473
Oy 476 E L L I I G A D L F Y G E O R G R V F I Y Q R - - - R O L G F E E V S E L Q D P G Y P L G R F G B A T I A L T D I 531
Db 474 D V L I G A P H Y E Q T R G G V S C P L P R G M R R M W C D A V - L Y G B Q G H P M G R F G A L T V L G D V 531
Oy 532 N G D G L V D A V A G A P L E O - - G A V Y I F N G H G - G L S P O P O R I E G T O V L S G I O M F G S I T G V 588
Db 532 N G D K L T D V I A P G E E N R G A V L F H G V L G P S I S P S H Q R I A G S Q L S S R L Q Y F G O A L S G G 591
Oy 589 K O L E G D G L A D V A G A S Q M I V L S R P V D M T L M S F S P A E I P V H E V E C S Y S T S N K M K E G V 648
Db 592 Q D L O D G L A V D A V A R G O V L I R T P V L M G V S M O F I A E I P R A S F E C R E O V A S E - Q T L V 650
Oy 649 N I T T C F O I K S I Y P O F O G R - - I V A N L T Y T L O D G H R T R R G L F P G G R H - E L R R N I A V T T S M 705
Db 651 Q S N I C L Y I D K S K N L G S R D L Q S V T L D L D P G L S P R A T Q E T K N S L S V R V L G K A 710
Oy 706 S C T D S S F R P V C V O D L I S P I N V S L N F S I M E E R G T R D R O A Q K D I P P I - L R P S I H S R - 761
Db 711 H C E N N L L P S C V E S E V P I T L R L N F T L - - - - - V G K P L A F R N I R P M L A A D Q 758
Oy 762 - - - T W E I P F E K N C G E D K C E A N L R V S F S P A R S A L R L A P A S L S V E L S I N L E E B A V W Q 818
Db 759 R Y F T A S L P F E K N C G A D H I C O D N L G I S F S P G L K S L I V G S N L E L N A V M W M D G E D S Y G T T 818
Oy 819 L D L F P P G L S F R K Y E M L K P H S Q - - - I P V S C E L P E S R L S R A L S C N V S P I F K A G H S V A 875
Db 819 I T F S H P A G L S Y R V A B G Q K O G L R E L H L T C S A P V G S Q - G T W S T S C R I N H I I F R G A Q I T 877
Oy 876 L O M M E N T I V N S S K G D S V E L H A N V T C N N E D S D L E N S A T T I - - - I P I L Y P I N I L I O D E D 932
Db 878 F L A A P P D V S P K A V L G D R L L L T A N V S E N N - - - T P R T S K T T P O L E L P V K Y A V T V V S S H E Q 933
Oy 933 S T L Y V S F T P K G P K - I H O V G H Y O V A I O P S I H D H N I P T - - - - - L E A V V G V 975
Db 934 F T K I T A N F E S E B E K S H V A M H R Y O V A - - - N L G O R D L P V S I N F V P V E L N O E A V M D V E V S H 990
Oy 976 P O P S E G B I T H O W S V O M E P V P C H E Y D E R L P D A E P C L P G A L - F R C P V - - - V F R O E I I V 1031
Db 991 P O N B S - - - - L R C S S E K I A P P A S D F L A H I Q K N P - V L D C S I A G L A R R C D V P S P S V G E I D F 1045
Oy 1032 Q V I G T L E L - - V E I F A S S M F S I C S L S I S F N S S K F H L Y G S N A S L A O V M K D V Y E E Q M 1089
Db 1046 T L K E N L S G W A R O I - L O K K V S V A S V A E I T P D T S V S O L P G O E A F M R - - - A Q T T V L E K Y K 1101
Oy 1090 L Y - - - - L V V L S I G G L L L L L I F I Y L Y V G P F K R L K E K M E A R G - - - V P N G - I P A D S 1140
Db 1102 V A N P P L V L G S S I G G L L L A L I T A V L Y V G F P K R O Y K E M E A N G O I A P E N G T O P S P S 1161
Oy 1141 E Q 1142
Db 1162 E K 1163

```

RESULT 13  
ITAD\_RAT

```

ID ITAD_RAT STANDARD; PRT; 1161 AA.
AC OQ9E7;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Integrin alpha-D precursor.
GN Name=Itgad;
OS Rattus norvegicus (Rat).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA O'Brien M.M., VanderVlieten M., Kilgannon P.D., Dietrich G.,
RA Gallatin W.M.;
RT "Cloning of rat alpha D, a novel beta 2 integrin.";
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Integrin alpha-D/beta-2 is a receptor for ICAM3 and
CC VCAM1. May play a role in the atherosclerotic process such as
CC clearing lipoproteins from plaques and in phagocytosis of blood-
CC borne pathogens, particulate matter, and senescent erythrocytes
CC from the blood (By similarity).
CC -1- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-D
CC associates with beta-2 (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins
CC with I-domains do not undergo protease cleavage.
CC -1- SIMILARITY: Belongs to the integrin alpha chain family.
CC -1- SIMILARITY: Contains 7 FG-GAP repeats.
CC -1- SIMILARITY: Contains 1 VWFA domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements/
CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; AF021354; AAF21241.1; -.
DR HSSP; P1215; 1BHQ.
DR InterPro; IPR000413; Integrin_alpha.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF01839; FG-GAP; 3.
DR Pfam; PF00357; Integrin_alpha; 1.
DR Pfam; PF00092; VWF; 1.
DR PRINTS; PRO0092; INTEGRIN.
DR PRINTS; PRO0453; VWFADOMAIN.
DR SMART; SM00327; VWF; 1.
DR SMART; PS00242; INTEGRIN_ALPHA; 1.
DR PROSITE; PS50234; VWFA; 1.
KW Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
KW Repeat; Signal; Transmembrane.
FT SIGNAL 1 19
FT CHAIN 20 1161
FT DOMAIN 20 1100
FT TRANSMEM 1101 1121
FT DOMAIN 1122 1161
FT REPEAT 34 87
FT REPEAT 88 7
FT REPEAT 152 334
FT REPEAT 352 402
FT REPEAT 403 454
FT REPEAT 456 517
FT REPEAT 519 577
FT REPEAT 582 634
FT CA_BIND 467 475
FT CA_BIND 531 539
FT CA_BIND 594 602
FT SITE 1126 1130
FT DISULFID 69 76

```

```

FT DISULFID 108 126 By similarity.
FT DISULFID 656 711 By similarity.
FT DISULFID 769 775 By similarity.
FT DISULFID 845 860 By similarity.
FT DISULFID 993 1017 By similarity.
FT DISULFID 1022 1027 By similarity.
FT CARBOHYD 61 61 N-linked (GlcNAc...) (potential).
FT CARBOHYD 89 89 N-linked (GlcNAc...) (potential).
FT CARBOHYD 245 245 N-linked (GlcNAc...) (potential).
FT CARBOHYD 393 393 N-linked (GlcNAc...) (potential).
FT CARBOHYD 696 696 N-linked (GlcNAc...) (potential).
FT CARBOHYD 734 734 N-linked (GlcNAc...) (potential).
FT CARBOHYD 784 784 N-linked (GlcNAc...) (potential).
FT CARBOHYD 907 907 N-linked (GlcNAc...) (potential).
FT CARBOHYD 936 936 N-linked (GlcNAc...) (potential).
FT CARBOHYD 1045 1045 N-linked (GlcNAc...) (potential).
SQ SEQUENCE 1161 AA; 126600 MW; 2258491A984705E CRC64;

Query Match 24.8%; Score 1516; DB 1; Length 1161;
Best Local Similarity 33.2%; Pred. No. 1.5e-90;
Matches 404; Conservative 207; Mismatches 465; Indels 142; Gaps 40;

13 LLSGFFFAVASSYNDVAGASSFPSPRAGRHYGVVLQVANG-VIVGAPGSG---NSTG 68
8 LLDG-WVLASCHGSNDVDEBPVIFREDAS--FGQTVVQFGSRLVVGAPLEAVANNQTG 64
69 SLVYOCGSGTGHCLPVTLRGS-NYSKYKLGMTLATDPTDGSIIACDGLSRTCDQNTYLSG 127
65 RLYDCAPATGMCOPVIRSPLEAVNMSTLSLTATNNAQLIACGPTQARACVKNMYAKG 124
128 LCVLPKRONLQSPMLQGR-GFOECIKGNVDFLPDGSMSLOPDEFQKLLDPMKMKKL 186
125 SCLLLAGSSLDQ--FTQVAPASMPCEPQEMDIAPLDGSGSINORDAKMDKVPKALMGF 182
187 SNTSYQFAVAPVOSTSYKTEFSDVYKRPDALLKGVKMLLTTFPAINYVATEVER 246
183 ASTSTLSLMQYNSLTKHTFTFEFNKIIDPOSVDPIYQGLGYTATGIRTWELFH 242
247 BEVKARPDATKVLIIITDG---EATDSGNIDAKD--IIRYIIGIHNPKTKESQETL 299
243 SKRGSRKSAKILVITTDQKRDPLEYSDVIRPADKAGIIRAIIVGAPQEPALKEI 302
300 HKFASRPAEFPVKILDTFEKLDLPTELQKTIYVTEGSKODLTSNMELSSSGISADLS 359
303 NTGSAAPQDHPFKVGNFALRSIQRLQEKI PALEGTSSRSSSQHMSQEGFSALT 362
360 RGHAVVAGVAGAKOMAGGFLDLKADLDODPTFIGNEPITPEVRAGYLGCTY--WLPSPROK 416
363 SDPVLGAVGFSWSGGAF-LYPRNTRPTFFIMSGENVMDSYLGSTPAVAFW----KG 417
417 TSLASGAPRYOMGRVLLFOBPQGGHMSOVQTIHGTOIGSYFGGELCGVVDODGETE 476
418 VNSLIGAPRRHQHTGVIF--TQEARHMRPKSEVAGTQIGVFASGLCSVDVDRGSD 475
477 LLLIGAPLYFGEGRGGRVITYO---RRDLGFEVSELOGDPGPIRGREGAITALTGIN 532
476 LVLLIGAPHYEQRGGQVSPFPVPGVRGMOCE--ATLHGEGOHGPRGVALTYLVDVN 533
533 GGGVAVVAVGAPLEEO--GAVYIIFNGRHG-GISPOSGRIEGQVLSGIOMVGRSIGHVK 589
534 GGNLADVALGAPGEERSRGAIVITFRASLLETMPSSQVNTSGLSLRLQITFGOSISGQ 593
590 DLGGDLADVAVGASQMTVLSRPVDMVTLMSPAPAI PVHEVACSYSSTNNKKEGVN 649
594 DLTQGLVAVLAVGAQGHVLLRLSLPLKLYELSLRFAFMVAVAKAVYQCMWERTPLVLEAG-E 652
650 IITICPKSLVYQFQGRRLVANLTYTLQLDGHRTRRGGLFGGRIHRIKRIATTSMS--- 706
653 ATVCLLVHKGSPDLGNVGSVRYDIALPBRGISATF-----DETAKCTLTGRKTLGL 707
707 ---CTDFSFHFPCVVDLSPINVSINFSLMEBEGPPROQAGKQIPIRLPSLSR-T 762
708 GHCEIVKLLPLDPCBDAVSPITLRNPLSVLVDASPR-----NLHVLAVGSDHIT 760

```

```

QY 763 WEIPKNGQEDKKCEANLAVSPSPARALRLTAPASLYELSLSNLEBDAYWQLDLH 822
DQ 761 ASLPEKNGCKQELLCEGDLGISFNFSGLQVLVGGSPPELITVYWNAGEBDSYGLTVFY 820
QY 823 FPPGLSPFRKVKMLKPHSQIP--VSCCELPEESRLRLALSCVNSPIPKAGSHVALQWVF 880
DQ 821 YNAGLSYRNVYTOQPHQPIRLACAPPAQEDL-RSSSCSINHPIRREGAKTFMTTF 879
DQ 881 NTLVNSWSDSVYELHANTCNNEEDLLEDNSATTI-IPILYPINILIQDQDSTLYVSF 939
DQ 880 DVSVAFLGDRLLRLAKKASSENNKED--TNKTAFLQELBPVKTYVTLISRGDSYTHNVF 937
QY 940 TPK-GEKIHQVKNVQVATQPSIHNDHNPITLNAVGVF-----QPSSE 981
DQ 938 SSSHGRRQEAHARRV-----NNLSPLKLAARVFWVPLLVGVAVMDVLTSSPQ 989
QY 982 GPITHQMSVQMPVY-PCHYEDLER--LPDAEBCPLGALPCPCVPRQETLVQVIGTL 1037
DQ 990 GV-----SCVSQMKFPQNPDLVQIQRRSVLDCSIADCLH---FRCD-----ISL 1032
QY 1038 ELVGEIE-----ASSMFSLCSLSISFNSKGFHLVGSNAST-AGVYMKV 1081
DQ 1033 DIQDELDFLNGNLSFGWVSQTLQEKVLVSBATIFPTSVYSQLPQGEAFLAQVETTL 1092
QY 1082 D--VYEEKQMLYLYLSGIGLILLLIFLYLYKGFPRKNIKEMEGRGVPGNIPAD 1139
DQ 1093 BEYVYEP--IFLVGSSVGGILLALITVLYLYKGFPRKYQKEMLD-----GKA 1140
QY 1140 SEQLASGOEAGPGGLXP 1157
DQ 1141 ADPVTAGQ--ADFGCETP 1156

```

```

RESULT 14
ID ITAM MOUSE STANDARD; PRT: 1153 AA.
AC P05555; O8CA73;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Integrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor MO1).
GN Name:Itgam;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=88312584; PubMed=3044779;
RA Pyela R.;
RT "Amino acid sequence of the murine Mac-1 alpha chain reveals homology with the integrin family and an additional domain related to von Willebrand factor";
RL EMBO J. 7:1371-1378(1988).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi U., Bono H., Kondo S., RA Nikaido I., Oeato N., Saito R., Suzuki H., Yamana H., Kiyosawa H., RA Yagi K., Tomaru Y., Haesgawa Y., Nogami A., Schonbach C., Gojobori T., RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., RA Schiml L.M., Kanapin A., Matsuda H., Batilov S., Beisel K.W., RA Blake J.A., Brad D., Brusic V., Chochia C., Corbani L.E., Cousins S., RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., RA Grimmond S., Gustigich S., Hirokawa N., Jackson I.J., Jarvis E.D., RA Kanai A., Kawai H., Kawasawa Y., Kedzierzki R.M., King B.L., RA Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., RA Nagashima T., Numata K., Okido T., Pavan W.J., Pesele G.,

```

RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sandelin A., Schneider C., Sempke C.A., Secou M., Shimada M.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
RA Vercaro R., Wagner L., Wahstedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carlini P., Hayatsu N.,  
RA Hironaka-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shitaki T., Waki K., Kawai K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Saesaki D., Shibata K., Shinagawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.,  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
[3]  
RP SEQUENCE OF 11-45 FROM N.A.  
RC STRAIN=BALB/c; TISSUE=Spleen;  
RX MEDLINE=86287312; PubMed=2942940;  
RA Sastre L., Roman J.M., Teplov D.B., Dreyer W.J., Gee C.E.,  
RA Larson R.S., Roberts T.M., Springer T.A.;  
RT "A partial genomic DNA clone for the alpha subunit of the mouse  
RT complement receptor type 3 and cellular adhesion molecule Mac-1.";  
RL Proc. Natl. Acad. Sci. U.S.A. 83:5644-5648(1986).  
[4]  
RP SEQUENCE OF 17-28.  
RX MEDLINE=85188276; PubMed=3887182;  
RA Springer T.A., Teplov D.B., Dreyer W.J.;  
RT "Sequence homology of the LFA-1 and Mac-1 leukocyte adhesion  
RT glycoproteins and unexpected relation to leukocyte interferon.";  
RL Nature 314:540-542(1985).  
CC -1- FUNCTION! Integrin alpha-M/beta-2 is implicated in various  
CC adhesive interactions of monocytes, macrophages and granulocytes  
CC as well as in mediating the uptake of complement-coated particles.  
CC It is identical with CR-3, the receptor for the IC3b fragment of  
CC the third complement component. It probably recognizes the R-G-D  
CC peptide in C3b. Integrin alpha-M/beta-2 is also a receptor for  
CC fibrinogen, factor X and ICAM1. It recognizes P1 and P2 peptides  
CC of fibrinogen gamma chain. Alpha-M/beta-2 play a critical role in  
CC mast cell development and in immune complex-mediated  
CC glomerulonephritis. Mice expressing a null mutation of the alpha-M  
CC subunit gene demonstrate increase in neutrophil accumulation, in  
CC response to a impaired degranulation and phagocytosis, events that  
CC apparently accelerate apoptosis in neutrophils. These mice develop  
CC obesity.  
CC -1- SUBUNIT: Heterodimer of an alpha and a beta chain. Alpha-M  
CC associates with beta-2.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=805555-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=805555-2; Sequence=VSP\_010473;  
CC Note=No experimental confirmation available;  
CC -1- TISSUE SPECIFICITY: Predominantly expressed in monocytes and  
CC granulocytes.  
CC -1- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins  
CC with I-domains do not undergo protease cleavage.  
CC -1- SIMILARITY: Belongs to the integrin alpha chain family.  
CC -1- SIMILARITY: Contains 7 FG-GAP repeats.  
CC -1- SIMILARITY: Contains 1 VWFA domain.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (see <http://www.ebi.ac.uk/announcements/>  
CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
CC -----  
CC EMBL; X07640; CAA30479.1; -.

DR EMBL; AK039444; BAC30350.1; -.  
DR EMBL; M14293; AAA39484.1; -.  
DR PIR; S00551; S00551.  
DR HSSP; P11215; 1BHO.  
DR MED; MG196607; ItgAm.  
DR GO; GO:0009897; C:external side of plasma membrane; IDA.  
DR GO; GO:0007155; P:cell adhesion; IMP.  
DR GO; GO:0045123; P:cellular extravasation; IMP.  
DR GO; GO:0030593; P:neutrophil chemotaxis; IMP.  
DR InterPro; IPR000413; Integrin\_alpha.  
DR InterPro; IPR002035; VWF\_A.  
DR Pfam; PF01839; FG-GAP; 3.  
DR Pfam; PF00357; Integrin\_alpha; 1.  
DR Pfam; PF00092; VWA; 1.  
DR PRINTS; PR01185; INTEGRINA.  
DR PRINTS; PR00453; VWFADOMAIN.  
DR SMART; SM00191; Itc\_alpha; 5.  
DR SMART; SM00327; VWA; 1.  
DR PROSITE; PS00242; INTEGRIN\_ALPHA; 1.  
DR PROSITE; PS0234; VWFA; 1.  
KW Alternative splicing; Calcium; Cell adhesion;  
KW Direct protein sequencing; Glycoprotein; Integrin; Receptor; Repeat;  
KW Signal; Transmembrane.  
FT SIGNAL 1 16  
FT CHAIN 17 1153  
FT DOMAIN 17 1105  
FT TRANSMEM 1106 1129  
FT DOMAIN 1130 1153  
FT REPEAT 31 84  
FT REPEAT 85 163  
FT REPEAT 164 350  
FT DOMAIN 337 400  
FT REPEAT 401 452  
FT REPEAT 454 515  
FT REPEAT 517 575  
FT REPEAT 580 632  
FT CA\_BIND 465 473  
FT CA\_BIND 529 537  
FT CA\_BIND 592 600  
FT SITE 1132 1136  
FT DISULFID 66 73  
FT DISULFID 105 123  
FT DISULFID 654 711  
FT DISULFID 770 776  
FT DISULFID 999 1023  
FT DISULFID 1028 1033  
FT CARBOHYD 58 58  
FT CARBOHYD 86 86  
FT CARBOHYD 391 391  
FT CARBOHYD 696 696  
FT CARBOHYD 734 734  
FT CARBOHYD 772 772  
FT CARBOHYD 801 801  
FT CARBOHYD 881 881  
FT CARBOHYD 907 907  
FT CARBOHYD 941 941  
FT CARBOHYD 980 980  
FT CARBOHYD 994 994  
FT CARBOHYD 1022 1022  
FT CARBOHYD 1045 1045  
FT CARBOHYD 1051 1051  
FT CARBOHYD 1076 1076  
FT VASPLIC 453 569  
FT -----  
FT CONFLICT 37 37  
FT CONFLICT 683 683  
SQ SEQUENCE 1153 AA; 127480 MW; 178DB98AECB0343 CRC64;  
Query Match 24.8%; Score 1514.5; DB 1; Length 1153;  
Best Local Similarity 33.8%; Pred. NO. 1.8e-90;  
Matches 407; Conservative 188; Mismatches 481; Indels 129; Gaps 36;  
QY 6 ITWAMALLSGFFAPASSYNLDVRCARSPSPRAGRHFYRVLYQV-GNGVIWVAPGEG 64

Db	6	LI.VT.LMALC.HGF-----	NLDTEHMTPEENAKG--	FGONVVGLGGSVVVAAR	QRA 54
Qy	65	---NSTGSLYQCSGTHCLPVTLR-	GSNVTSGKYLGMTLPTDSDIS	LACDGLSRTCD	120
Db	55	KAVNOTGALYQCDYSTRCHPIPLQV	PRPAVNMISLISLAVTVPOOL	LACSPYTHQNK 114	
Qy	121	ONTYLSGLCYLFRONLQGMLOGR	PGFOECSIKANDVLELFDGSM	SLQDRFOKILDFMK 180	
Db	115	ENTYVNGLCYLFSGNMLRPRQGF	PRALRBCPOQESDIFVLIDGSG	SININDFQKMEFYS 174	
Qy	161	DYMKLSNTSYQPAVQFSTKYTBED	SEDDYKRRDPDALLKYNKMLLT	ITTFGALINY 240	
Db	175	TYMEOFKSKSTFLSMLOQYDEPR	INHTFDFPKNPSRSHVSPIKOL	NRRTYKASGIRYV 234	
Qy	241	ATEVPREELGAPRDATKVLIIITD	GE-----ATDSCNIDAADK---	IIRYITIGIKHFORK 293	
Db	235	VARELHNTKGAENNAKILVITDGE	KFPDPLDYKQVIREADRAGYIR	VYIGANFNKR 294	
Qy	294	ESQETLHKRASKRASEFVKILDT	PEKLDLTELQKKIVIEBTSKOD	ITSPFMELSSSG 353	
Db	295	QSRRELDITASRPAQHNVQVND	FALNTIQLODEKIPALISTQ	GTSGTSSFEHNSQSG 354	
Qy	354	ISADLSRGHAVVANGAKDWAGG-	FLDLKADLODFTIGNBPLTEV	RAGYIGYTYTLR 412	
Db	355	FSASITSGPILGSGSPDMAGAF	LYTSKD--KVFINTTVDSDMNA	YUIGYASAVI- 411	
Qy	413	SRQKTSILASGAPRYOHMGRVLL	FPQROGGHMSQVQTIHNGIQS	YFGGELCGVDD 472	
Db	412	LNRKQSVLVAQPRYOHIGLVVMP	RE--NFGTWEPHTISIKSQIS	YFASILCSYMDAD 469	
Qy	473	GETELLLIGAPLFYEBORGARVFI-	YORROIGFEEVSLQSDPYPLR	FGGALITALD 530	
Db	470	GNTNLILIGAPHYEKTGGQVSVCL	PRGPARMOGBALHEDQHMPK	RFGALITVLGD 529	
Qy	531	INQDGLVDVAVAP--LEBQAGVYI	FNNGH--GGLSPQSPQRIE	GTQVLSGIQWFGHSIHG 587	
Db	530	VNGDKLTVALIAGPEBOENQAGV	IFYGASISLASHHRITIGA	PSGLQYFGQSLSG 589	
Qy	588	VKDLEGGDLADVAVABESOMITL	SRPVDMTILMSFSAELRYNEH	VECSYSTSNMKEG 647	
Db	590	GKDLTMDGMDLDAVAGQGLLRL	ROPVLRALPATEFSPSKAR	SVPAQEOVL--NKKA 648	
Qy	648	VNITTCFOIKSLYPO--FQGR	LVANITYLLOLGHTRRGGLF	PGGRHLEARNIATYSM 705	
Db	649	GEVRGCLARKNTXORLREGDI	QSYTYTVDLADPRASRI	RAFDEKONTRRTQVFGLM 708	
Qy	706	-SCTDPSFHFVYCVODLSP	IVNLSNFSIMEEBGTPRDQ	AKOIPILRPSLSE-- 761	
Db	709	QKCEITAKLILPCQVDSDV	SPILRLNLYTL--VGEPR--	LRFSGN-----LRPLVMDAQR 758	
Qy	762	---TWETIPEKNGGDEKCKGAN	LRVSPRSALRLITAPASIS	VELSLESTNLEBDATVUD 819	
Db	759	FFTANFPPEKNGSNDISICQD	DLSTMSAMGLDTLVVGGP	QDPMNSVTLNDDSDSGTY 818	
Qy	820	DLHFPFGSGFRKYEMLKPHSOI	PVSGEE--LPESSRLSS-----	RALSCHVSSPIFXA 870	
Db	819	TVIYVSSGSLYK---DSASQ	NPLTKKPFYVAPRASSSS	SEBGALKSTTNMINHPIPA 874	
Qy	871	GHSVALQMMFNTLVNSSWGD	SVELHANVTCNNEDBDL-----	LEBDSATIIIPILYPTN 924	
Db	875	NSBVTFNVTYFDVDSHAS	FGNKLKLLKALIVASENNMS	RTHKTKFOLE-----LPVXALY 927	
Qy	925	ILIDQOEDSTLVSTTPKGR	KTHQKMYQVAILQSIHINHNI	PYLEAVGVGVQRPBEGGI 984	
Db	928	MTIVSDESSIRYLNFTASE	MTSKVIOHQOFN--NLQGR	SILP--VSVMWIPQOINNTV 983	
Qy	985	THQW-----SVQMEBPV	CHYEDLERLDAABPCLP	GAALFPCQPVF--- 1022	
Db	984	---WHHPQVIFSQNLSSACH	TQEKQRPBHNPRDQLERT-----	VANCSAVAVCR 103	
Qy	1026	---ROEIL--VOYITGLV	ELVGEILBAS--SMFSLCS	SLSISFNSSGHFLYGSNGL 107	

Dd		1031	IQCPLPSEFNTIOELINVTILKGNLSFDWTYIKTSHGILLVSVSTIELIFDNDSPALLPGQSYV	1090
Oy		1075	-AQQVMKVDDVYEKKOMLYLVYLSCIGIGLLLLLFIIVLYKVGFKPKRM,KEKMEAGRGVPN	1133
Dd		1091	RSKETIEKYEPPEVANNPPVLIVGSSITGLVILLALITAGLYTLGFFKRQYKOMM--NEAAPQ	1148
Oy		1134	GIPAE 1138	
Dd		1149	DAPQ 1153	
 RESULT 15				
O9J130				
ID	Q9J130	PREDIMINARY;	PRT; 1151 AA.	
AC	Q9J130;			
DT	01-OCT-2000	(TREMBLrel. 15, Created)		
DT	01-OCT-2000	(TREMBLrel. 15, Last sequence update)		
DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)		
DE		Integrin beta 2 alpha subunit.		
OS		Rattus norvegicus (Rat).		
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCHI_TaxId=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Fathallah D.M. Sr., Zeria K. Jr.;			
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.			
CC	-I- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).			
CC	-I- SIMILARITY: Belongs to the integrin alpha chain family.			
DR	EMBL; AF268553; AAPB1280.1; --.			
DR	HSSP; P11215; IBHQ.			
DR	GO; GO:0016021; C:integral to membrane; IEA.			
DR	GO; GO:0008305; C:integrin complex; IEA.			
DR	GO; GO:0005515; F:protein binding; IEA.			
DR	GO; GO:0007160; P:cell-matrix adhesion; IEA.			
DR	GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.			
DR	InterPro; IPRO00413; Integrin_alpha.			
DR	InterPro; IPRO2035; VWF_A.			
DR	Pfam; PF00357; Integrin_alpha; 1.			
DR	Pfam; PF00357; VWA; 1.			
DR	PRINTS; PRO1182; INTEGRINA.			
DR	PRINTS; PRO0453; VWPADOMAIN.			
DR	SMART; SMO0193; Int_alpha; 5.			
DR	SMART; SMO0327; VWA_1.			
DR	PROSITE; PS00242; INTEGRIN_ALPHA; 1.			
DR	PROSITE; PS00243; VWF_A; 1.			
KW	Cell adhesion; Integrin; Transmembrane.			
SQ	SEQUENCE 1151 AA; 126943 MW; 8PF85695PD4074C4S CRC64;			
 Query Match 24.4%; Score 1488.5; DB 2; Length 1151;				
Best Local Similarity 33.7%; Pred. No. 9.3e-89;				
Matches 395; Conservative 193; Mismatches 471; Indels 113; Gaps 34;				
Oy		26	YNLDVRGARSRFPARRGRHFGYRLVQNG-NGVIVGAPGE---GNSTSLYCQCGSGTGHL	81
Dd		17	FNLDTENPMPTFOEASG--FGQSVIQGGERVVVAAPQAKVANQTALVQCDYSTRKCD	74
Oy		82	PVTLR-GSNYSKTYLGMTLATDPTDGSIACDPGLSFRTCDQNTYLSGLCYLPFRONTIGPM	140
Dd		75	PILPVPPPAVNMSISGLSLAATTVPPQLLAGCPFHVNCNKENTYVNLGYLFCSNLLRKP	134
Oy		141	LQGPRGQECIKGNVDLVFLPDSMSLQPBEPKIIDFMEDWKVKLSNSTSYGAAYOFST	200
Dd		135	QQPPEALRGCCQOESNAFLIDSGSINTIIDFQMKEFVSVTDMDQFOKSXTLLPSLMQYSD	194
Oy		201	SYKTEPDFSDYVVRKKDDALDKHKMLLTNTFGAINVYAATEVFRELGGARPDAATKVI	260
Dd		195	EFRRHFNFNDPCKNRDPDKSHVRIPLQNGRTKTASGIRKRVRELPQINGARDMAAKIIIV	254
Oy		261	IITDG-----EATSGNIDAAKOIIRIYIGIGKGFKQTESGETLHKASKP	306
Dd		255	VITDEKEFGDPLNVIEDVIPAEARG-----IIRVYIGVGNAFHNQRSRELDITJASKP	307





GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 29, 2005, 19:19:14 ; Search time 178 Seconds  
(without alignments)  
2582.717 Million cell updates/sec

Title: US-09-945-265-2

Perfect score: 6106

Sequence: 1 MKDSCITMAMALLSGFFP.....DRCGLKPHKSDSGGKRD 1170

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1767149 seqs, 392926209 residues

1767149

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_NEW\_PUB.pep:\*  
12: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*  
17: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*  
18: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*  
19: /cgn2\_6/ptodata/2/pubpaa/US11A\_PUBCOMB.pep:\*  
20: /cgn2\_6/ptodata/2/pubpaa/US11A\_NEW\_PUB.pep:\*  
21: /cgn2\_6/ptodata/2/pubpaa/US11A\_NEW\_PUB.pep:\*  
22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6106	100.0	1170	9	US-09-945-265-2
2	6106	100.0	1170	16	US-10-473-127-1743
3	6098	99.9	1170	15	US-10-261-164-1
4	6098	99.9	1170	16	US-10-473-127-1737
5	6098	99.9	1170	16	US-10-473-127-1739
6	6098	99.9	1170	16	US-10-473-127-1742
7	6098	99.9	1170	16	US-10-741-600-1088
8	6061.5	99.3	1170	20	US-11-062-290-1
9	6061.5	99.3	1223	17	US-10-741-600-1086
10	6053.5	99.1	1223	16	US-10-408-765A-295
11	6053.5	99.1	1223	16	US-10-473-127-1736

12	5981	98.0	1145	17	US-10-872-198-130	Sequence 130, App
13	5981	98.0	1145	20	US-11-021-951-130	Sequence 130, App
14	5973	97.8	1145	16	US-10-473-127-1738	Sequence 1738, App
15	5649.5	92.5	1086	16	US-10-473-127-1741	Sequence 1741, App
16	5585	91.5	1086	16	US-10-408-765A-1871	Sequence 1871, App
17	5585	91.5	1086	16	US-10-473-127-1735	Sequence 1735, App
18	5585	91.5	1086	16	US-10-473-127-1744	Sequence 1744, App
19	5585	91.5	1086	17	US-10-741-600-1087	Sequence 1087, App
20	5533.5	90.6	1065	16	US-10-473-127-1740	Sequence 1740, App
21	3066	50.2	589	15	US-10-261-164-2	Sequence 2, Appl1
22	3066	50.2	589	20	US-11-062-290-2	Sequence 2, Appl1
23	1563	25.6	1153	9	US-09-350-259-3	Sequence 3, Appl1
24	1563	25.6	1153	10	US-09-902-481A-1	Sequence 1, Appl1
25	1563	25.6	1153	10	US-09-891-943-3	Sequence 3, Appl1
26	1563	25.6	1153	14	US-10-144-259-30	Sequence 30, Appl1
27	1563	25.6	1153	14	US-10-207-655-176	Sequence 176, App
28	1567.5	25.5	1137	10	US-09-945-265-4	Sequence 4, Appl1
29	1557.5	25.5	1137	10	US-09-902-481A-5	Sequence 5, Appl1
30	1557.5	25.4	1137	10	US-09-902-481A-6	Sequence 6, Appl1
31	1547.5	25.3	1137	10	US-09-902-481A-4	Sequence 4, Appl1
32	1536.5	25.2	1137	10	US-09-902-481A-3	Sequence 4, Appl1
33	1521.5	24.9	1163	15	US-10-116-275-204	Sequence 204, App
34	1521.5	24.9	1163	16	US-10-723-660-327	Sequence 327, App
35	1515.5	24.8	1163	18	US-10-794-899-100	Sequence 100, App
36	1504	24.6	1161	9	US-09-350-259-55	Sequence 55, Appl1
37	1504	24.6	1161	10	US-09-891-943-55	Sequence 53, Appl1
38	1490	24.4	1161	9	US-09-350-259-53	Sequence 53, Appl1
39	1490	24.4	1161	10	US-09-891-943-53	Sequence 53, Appl1
40	1480.5	24.2	1163	10	US-09-350-259-4	Sequence 4, Appl1
41	1480.5	24.2	1163	10	US-09-891-943-4	Sequence 4, Appl1
42	1476	24.2	1161	9	US-09-350-259-9	Sequence 2, Appl1
43	1476	24.2	1161	10	US-09-891-943-2	Sequence 2, Appl1
44	1475.5	24.2	1161	9	US-09-350-259-99	Sequence 99, Appl1
45	1475.5	24.2	1161	10	US-09-891-943-99	Sequence 99, Appl1

#### ALIGNMENTS

RESULT 1  
US-09-945-265-2  
Sequence 2, Appl1 US/09945265  
Patent No. US20020123614A1  
GENERAL INFORMATION:  
APPLICANT: Springer, Timothy A.  
APPLICANT: Shimadzu, Mocomu  
APPLICANT: Iu, Chafin  
TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A  
FILE REFERENCE: CEN-002CP  
CURRENT APPLICATION NUMBER: US/09/945, 265  
CURRENT FILING DATE: 2001-08-31  
PRIOR APPLICATION NUMBER: US 60/229, 700  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 1170  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-945-265-2

Query Match 100.0%; Score 6106; DB 9; Length 1170;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKDSCITMAMALLSGFFFPASSYNDVAGASFPSPRGRFRGVYGVGA 60  
DB 1 MKDSCITMAMALLSGFFFPASSYNDVAGASFPSPRGRFRGVYGVGA 60  
QY PGEAGSTSLVQCOSGTHCLPVLTRGSNTSKYLGMTIATDPDGSIIACDPGLSTRCD 120  
DB PGEAGSTSLVQCOSGTHCLPVLTRGSNTSKYLGMTIATDPDGSIIACDPGLSTRCD 120

121 QNTYLSGLCYLFRONLOGPMLQGRPGFOECIKGNVDLVEFLFDGSMLSQDPDEFOKILDFPMK 180  
121 QNTYLSGLCYLFRONLOGPMLQGRPGFOECIKGNVDLVEFLFDGSMLSQDPDEFOKILDFPMK 180  
181 DVMKLSNTSYQFAAVQFSTSYKTEPDSYVKRDPALLKHYKMLLLTNTFGAINYV 240  
181 DVMKLSNTSYQFAAVQFSTSYKTEPDSYVKRDPALLKHYKMLLLTNTFGAINYV 240  
241 ATEVFRBELGARPDATKVLIIITDGEATDSGNIDAADRIIYIIGIKHQTESQETLH 300  
241 ATEVFRBELGARPDATKVLIIITDGEATDSGNIDAADRIIYIIGIKHQTESQETLH 300  
301 KFASKPASEFVKILDTFEKLDLFTLEOKKIYVIBGTSKODLTSFNMELSSSGISADLSR 360  
301 KFASKPASEFVKILDTFEKLDLFTLEOKKIYVIBGTSKODLTSFNMELSSSGISADLSR 360  
361 GHAVVAVGAKDWAAGFLDLKADLQDDTFIGNEPITPEVRAGYLGVTVMWPSROKTSLL 420  
361 GHAVVAVGAKDWAAGFLDLKADLQDDTFIGNEPITPEVRAGYLGVTVMWPSROKTSLL 420  
421 ASGAPRYOHMGRVLLFOEPQGGHWSQVQTIHGTOIGSYFGEELCGVDVDDGETELLII 480  
421 ASGAPRYOHMGRVLLFOEPQGGHWSQVQTIHGTOIGSYFGEELCGVDVDDGETELLII 480  
481 GAPLFYEGORGRVFIYORROLGFEFVSELQDPPGYPLGRFGAITALTDINGDLVDVA 540  
481 GAPLFYEGORGRVFIYORROLGFEFVSELQDPPGYPLGRFGAITALTDINGDLVDVA 540  
541 VGAPLEBOGAVYIFNGRHGSLPOPSQRIEGTOVLSGIQWFGRSIHGVKLEBGLADVA 600  
541 VGAPLEBOGAVYIFNGRHGSLPOPSQRIEGTOVLSGIQWFGRSIHGVKLEBGLADVA 600  
541 VGAPLEBOGAVYIFNGRHGSLPOPSQRIEGTOVLSGIQWFGRSIHGVKLEBGLADVA 600  
601 VGASQOMVLSRPVDMVTLMSPAPIPVHEVCSTSTSNKMEGNITICQIKSLY 660  
601 VGASQOMVLSRPVDMVTLMSPAPIPVHEVCSTSTSNKMEGNITICQIKSLY 660  
661 POFQGRIVANTLYTLQDGHRTRRRGLPPGGRHRLRRIIAVTTSMCTDFSFHPVVCOD 720  
661 POFQGRIVANTLYTLQDGHRTRRRGLPPGGRHRLRRIIAVTTSMCTDFSFHPVVCOD 720  
721 LISPIVNSLNSLWEEBGTPRDQRAQKODIPPIILPILSHSTWBIPEFKNCGEBKCEAN 780  
721 LISPIVNSLNSLWEEBGTPRDQRAQKODIPPIILPILSHSTWBIPEFKNCGEBKCEAN 780  
781 LRVSPSPRSRALRLTAFASLSVELSTLSNLEBDAYWQDLHFPPGLSFRKVMKXPHSQ 840  
781 LRVSPSPRSRALRLTAFASLSVELSTLSNLEBDAYWQDLHFPPGLSFRKVMKXPHSQ 840  
841 IPVCEBELPEESRLSRALSCNVSSPIFKAGSHVALQMMFNTLVNWSWGDSEVELHANVTC 900  
841 IPVCEBELPEESRLSRALSCNVSSPIFKAGSHVALQMMFNTLVNWSWGDSEVELHANVTC 900  
901 NNEBSDLIEDNSATTIPIILYPINILQDQEDSTLYVFTPKGPKIHQVKMYOVR1OPS 960  
901 NNEBSDLIEDNSATTIPIILYPINILQDQEDSTLYVFTPKGPKIHQVKMYOVR1OPS 960  
961 IHDNIPITLNAVGVQPPSPSGPITTHQMSVQMEPPVPHYEDLEBLPMAAPCPLGALFR 1020  
961 IHDNIPITLNAVGVQPPSPSGPITTHQMSVQMEPPVPHYEDLEBLPMAAPCPLGALFR 1020  
1021 CPVVFROEILVQVIGTLELVEIEIKASWFSLSLSSISIFNSSKIFHLVGSNALSQAQVVMK 1080  
1021 CPVVFROEILVQVIGTLELVEIEIKASWFSLSLSSISIFNSSKIFHLVGSNALSQAQVVMK 1080  
1081 DVVAVYKQMLLYLVLSGIGLILLLLIFIVLYKXGFFRRNDKEROMAGRGVPPNGIPAEBS 1140  
1081 DVVAVYKQMLLYLVLSGIGLILLLLIFIVLYKXGFFRRNDKEROMAGRGVPPNGIPAEBS 1140  
1141 EQLASGOBAGDPCCLKPLHEKDSBGGGKD 1170  
1141 EQLASGOBAGDPCCLKPLHEKDSBGGGKD 1170  
1141 EQLASGOBAGDPCCLKPLHEKDSBGGGKD 1170

RESULT 2  
US-10-473-127-1743  
; Sequence 1743, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473.127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1743  
; LENGTH: 1170  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1743

Query Match 100.0%; Score 6106; DB 16; Length 1170;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKDSCITVMAMALLSGFFFPAPASYNLDVRGARSFSPPRAGHFGYRVLQVANGVIVGA 60  
DB 1 MKDSCITVMAMALLSGFFFPAPASYNLDVRGARSFSPPRAGHFGYRVLQVANGVIVGA 60  
QY 61 PGEBSNSTGSLYOCOSGTGHCLPTVTLKGSNTSKYLQMTLATDPTDGSIIACDPLSRTCD 120  
DB 61 PGEBSNSTGSLYOCOSGTGHCLPTVTLKGSNTSKYLQMTLATDPTDGSIIACDPLSRTCD 120  
QY 121 QNTYLSGLCYLFRONLOGPMLQGRPGFOECIKGNVDLVEFLFDGSMLSQDPDEFOKILDFPMK 180  
DB 121 QNTYLSGLCYLFRONLOGPMLQGRPGFOECIKGNVDLVEFLFDGSMLSQDPDEFOKILDFPMK 180  
QY 181 DVMKLSNTSYQFAAVQFSTSYKTEPDSYVKRDPALLKHYKMLLLTNTFGAINYV 240  
DB 181 DVMKLSNTSYQFAAVQFSTSYKTEPDSYVKRDPALLKHYKMLLLTNTFGAINYV 240  
QY 241 ATEVFRBELGARPDATKVLIIITDGEATDSGNIDAADRIIYIIGIKHQTESQETLH 300  
DB 241 ATEVFRBELGARPDATKVLIIITDGEATDSGNIDAADRIIYIIGIKHQTESQETLH 300  
QY 301 KFASKPASEFVKILDTFEKLDLFTLEOKKIYVIBGTSKODLTSFNMELSSSGISADLSR 360  
DB 301 KFASKPASEFVKILDTFEKLDLFTLEOKKIYVIBGTSKODLTSFNMELSSSGISADLSR 360  
QY 361 GHAVVAVGAKDWAAGFLDLKADLQDDTFIGNEPITPEVRAGYLGVTVMWPSROKTSLL 420  
DB 361 GHAVVAVGAKDWAAGFLDLKADLQDDTFIGNEPITPEVRAGYLGVTVMWPSROKTSLL 420  
QY 421 ASGAPRYOHMGRVLLFOEPQGGHWSQVQTIHGTOIGSYFGEELCGVDVDDGETELLII 480  
DB 421 ASGAPRYOHMGRVLLFOEPQGGHWSQVQTIHGTOIGSYFGEELCGVDVDDGETELLII 480  
QY 481 GAPLFYEGORGRVFIYORROLGFEFVSELQDPPGYPLGRFGAITALTDINGDLVDVA 540  
DB 481 GAPLFYEGORGRVFIYORROLGFEFVSELQDPPGYPLGRFGAITALTDINGDLVDVA 540  
QY 541 VGAPLEBOGAVYIFNGRHGSLPOPSQRIEGTOVLSGIQWFGRSIHGVKLEBGLADVA 600  
DB 541 VGAPLEBOGAVYIFNGRHGSLPOPSQRIEGTOVLSGIQWFGRSIHGVKLEBGLADVA 600

Db 541 VGAPLEBQAGVYIFNGRHGGLSPQPSQRIEGTVLSGIQWFGRSIHGVKDLBEGDLADVA 600  
Qy 601 VGASEQMTVLSSRPVVDWMTLMSFPAEIPVHEVCSTSTSNKMEGVNITICFOIKSLY 660  
Db 601 VGASEQMTVLSSRPVVDWMTLMSFPAEIPVHEVCSTSTSNKMEGVNITICFOIKSLY 660  
Qy 661 POFQGRIVANITVTLQDGHRTTRRGLPPGGRHRLRNIAVTTSMSCDTSFHFVVCQD 720  
Db 661 POFQGRIVANITVTLQDGHRTTRRGLPPGGRHRLRNIAVTTSMSCDTSFHFVVCQD 720  
Qy 721 LISPIVNSLNSLMEEBGTPRDQAOQKDIPEILPRLSHSETWEIPFEKNGCEKCCBAN 780  
Db 721 LISPIVNSLNSLMEEBGTPRDQAOQKDIPEILPRLSHSETWEIPFEKNGCEKCCBAN 780  
Qy 781 LRVSPSPARSRLRLTAFASLSVSLSNLEEDAWVQDLHFPGLSFRKYEMLKPHSQ 840  
Db 781 LRVSPSPARSRLRLTAFASLSVSLSNLEEDAWVQDLHFPGLSFRKYEMLKPHSQ 840  
Qy 841 IPVSCBELPEBSRLLSRALSCNVSSPIFKAGHSVALQMMFNTLVNSWGDVVELHANVTC 900  
Db 841 IPVSCBELPEBSRLLSRALSCNVSSPIFKAGHSVALQMMFNTLVNSWGDVVELHANVTC 900  
Qy 901 NNBSDDLSDNSATTIIPILYPINILIQDEDSITVYFTPKGPKIHQVKMYQVRIOPS 960  
Db 901 NNBSDDLSDNSATTIIPILYPINILIQDEDSITVYFTPKGPKIHQVKMYQVRIOPS 960  
Qy 961 IHDNIPITLBAVVGVPQPSSEGPITTHQMSVQMEPPVCHYEDLERLPDAEPCLPGALFR 1020  
Db 961 IHDNIPITLBAVVGVPQPSSEGPITTHQMSVQMEPPVCHYEDLERLPDAEPCLPGALFR 1020  
Qy 1021 CPVVFROEILVQVIGTLELVGEIEBASMFSLCSSLSTISFNSSKHHLVGSNASLAQVYMK 1080  
Db 1021 CPVVFROEILVQVIGTLELVGEIEBASMFSLCSSLSTISFNSSKHHLVGSNASLAQVYMK 1080  
Qy 1081 VDVIYKEMQMLYLYLSGIGLLLLLFIVLYKVGFPRKRLKEXMEAGRGVPNGI PAEDS 1140  
Db 1081 VDVIYKEMQMLYLYLSGIGLLLLLFIVLYKVGFPRKRLKEXMEAGRGVPNGI PAEDS 1140  
Qy 1141 EQLASQAGADPGCLKPLHEKDSGSGXKD 1170  
Db 1141 EQLASQAGADPGCLKPLHEKDSGSGXKD 1170

RESULT 3  
US-10-261-164-1  
; Sequence 1, Application US/10261164  
; Publication No. US20040062765A1  
; GENERAL INFORMATION:  
; APPLICANT: KAPUSTAY, PAMELA M.  
; APPLICANT: LEWIS, REX H.  
; TITLE OF INVENTION: LPA-1 ALPHA SUBUNIT ANTIBODIES AND METHODS OF USE  
; FILE REFERENCE: 046007/0272304  
; CURRENT APPLICATION NUMBER: US/10/261,164  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1170  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-261-164-1

Query Match 99.9%; Score 6098; DB 15; Length 1170;  
Best Local Similarity 99.9%; Pred. 0;  
Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKDSCTTMAAMALLSGFFFPAPASYNIDVGARFSFPPRAGRHHGVLYQVNGVYIGA 60  
Db 1 MKDSCTTMAAMALLSGFFFPAPASYNIDVGARFSFPPRAGRHHGVLYQVNGVYIGA 60  
Qy 61 PGEKSTSLVQCCSGTGCHLPVTLRGSNTYSKYLGMTLATDPTDGSILACDPGLSRTCD 120  
Db 61 PGEKSTSLVQCCSGTGCHLPVTLRGSNTYSKYLGMTLATDPTDGSILACDPGLSRTCD 120

Qy 121 ONTVLSGICVTLFRONLOQPMLOGRPGFOECLKGNVDLVFLPDGSMSLQPDFOKILDPMK 180  
Db 121 ONTVLSGICVTLFRONLOQPMLOGRPGFOECLKGNVDLVFLPDGSMSLQPDFOKILDPMK 180  
Qy 181 DVMKGLSNTSYQFAAVQFSTSYKTEPDFSDVKKKDDALLAKHYKMLLNTNGAINVY 240  
Db 181 DVMKGLSNTSYQFAAVQFSTSYKTEPDFSDVKKKDDALLAKHYKMLLNTNGAINVY 240  
Qy 241 ATEVFRBELGARPDATVYLIIITDGEATDGSNIDAANDIIRYIIIGIKHFOTKESQETLH 300  
Db 241 ATEVFRBELGARPDATVYLIIITDGEATDGSNIDAANDIIRYIIIGIKHFOTKESQETLH 300  
Qy 301 KFAKSPASEFYKILIDTEBKLKOLFTELOKTIYVEIGTSKODLTSPNNELSSGISAIDLK 360  
Db 301 KFAKSPASEFYKILIDTEBKLKOLFTELOKTIYVEIGTSKODLTSPNNELSSGISAIDLK 360  
Qy 361 GHAVVAVGAKDMAGGFJDLKADLQDDPTFGNEBLTEBVRAGVLYGYTVMPLPSRQKTSIL 420  
Db 361 GHAVVAVGAKDMAGGFJDLKADLQDDPTFGNEBLTEBVRAGVLYGYTVMPLPSRQKTSIL 420  
Qy 421 ASGAPRYQHMGRVLLFOEPQGGHMSQVOTIHGTQISYFGBELCGVDVDDGETELLII 480  
Db 421 ASGAPRYQHMGRVLLFOEPQGGHMSQVOTIHGTQISYFGBELCGVDVDDGETELLII 480  
Qy 481 GAPLFYGBQRGGRVFIYQRRQLGFEVSELOQDPGYLGRFGELITALTDINGGLYDVA 540  
Db 481 GAPLFYGBQRGGRVFIYQRRQLGFEVSELOQDPGYLGRFGELITALTDINGGLYDVA 540  
Qy 541 VGAPLEBQAGVYIFNGRHGGLSPQPSQRIEGTVLSGIQWFGRSIHGVKDLBEGDLADVA 600  
Db 541 VGAPLEBQAGVYIFNGRHGGLSPQPSQRIEGTVLSGIQWFGRSIHGVKDLBEGDLADVA 600  
Qy 601 VGASEQMTVLSSRPVVDWMTLMSFPAEIPVHEVCSTSTSNKMEGVNITICFOIKSLY 660  
Db 601 VGASEQMTVLSSRPVVDWMTLMSFPAEIPVHEVCSTSTSNKMEGVNITICFOIKSLY 660  
Qy 661 POFQGRIVANITVTLQDGHRTTRRGLPPGGRHRLRNIAVTTSMSCDTSFHFVVCQD 720  
Db 661 POFQGRIVANITVTLQDGHRTTRRGLPPGGRHRLRNIAVTTSMSCDTSFHFVVCQD 720  
Qy 721 LISPIVNSLNSLMEEBGTPRDQAOQKDIPEILPRLSHSETWEIPFEKNGCEKCCBAN 780  
Db 721 LISPIVNSLNSLMEEBGTPRDQAOQKDIPEILPRLSHSETWEIPFEKNGCEKCCBAN 780  
Qy 781 LRVSPSPARSRLRLTAFASLSVSLSNLEEDAWVQDLHFPGLSFRKYEMLKPHSQ 840  
Db 781 LRVSPSPARSRLRLTAFASLSVSLSNLEEDAWVQDLHFPGLSFRKYEMLKPHSQ 840  
Qy 841 IPVSCBELPEBSRLLSRALSCNVSSPIFKAGHSVALQMMFNTLVNSWGDVVELHANVTC 900  
Db 841 IPVSCBELPEBSRLLSRALSCNVSSPIFKAGHSVALQMMFNTLVNSWGDVVELHANVTC 900  
Qy 901 NNBSDDLSDNSATTIIPILYPINILIQDEDSITVYFTPKGPKIHQVKMYQVRIOPS 960  
Db 901 NNBSDDLSDNSATTIIPILYPINILIQDEDSITVYFTPKGPKIHQVKMYQVRIOPS 960  
Qy 961 IHDNIPITLBAVVGVPQPSSEGPITTHQMSVQMEPPVCHYEDLERLPDAEPCLPGALFR 1020  
Db 961 IHDNIPITLBAVVGVPQPSSEGPITTHQMSVQMEPPVCHYEDLERLPDAEPCLPGALFR 1020  
Qy 1021 CPVVFROEILVQVIGTLELVGEIEBASMFSLCSSLSTISFNSSKHHLVGSNASLAQVYMK 1080  
Db 1021 CPVVFROEILVQVIGTLELVGEIEBASMFSLCSSLSTISFNSSKHHLVGSNASLAQVYMK 1080  
Qy 1081 VDVIYKEMQMLYLYLSGIGLLLLLFIVLYKVGFPRKRLKEXMEAGRGVPNGI PAEDS 1140  
Db 1081 VDVIYKEMQMLYLYLSGIGLLLLLFIVLYKVGFPRKRLKEXMEAGRGVPNGI PAEDS 1140  
Qy 1141 EQLASQAGADPGCLKPLHEKDSGSGXKD 1170  
Db 1141 EQLASQAGADPGCLKPLHEKDSGSGXKD 1170

RESULT 4  
US-10-473-127-1737  
; Sequence 1737, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1737  
; LENGTH: 1170  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1737

Query Match 99.9%; Score 6098; DB 16; Length 1170;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKDSCITYAMALLSGFFFAFPASSYNLDVGRARSFSPRAGRHRFGYVLOVANGVIYGA 60  
DB 1 MKDSCITYAMALLSGFFFAFPASSYNLDVGRARSFSPRAGRHRFGYVLOVANGVIYGA 60  
QY 61 PGEAGNSTSLYQCCSGTGHCLPVTLRGSNYSKYLGMTLADPTDGSILACDPGLSRICD 120  
DB 61 PGEAGNSTSLYQCCSGTGHCLPVTLRGSNYSKYLGMTLADPTDGSILACDPGLSRICD 120  
QY 121 QNTYLSGLCYLFRQNLQGPMLQGRPGFOCIKGNVDLVELFDGSMSLQPDFOKILDFMK 180  
DB 121 QNTYLSGLCYLFRQNLQGPMLQGRPGFOCIKGNVDLVELFDGSMSLQPDFOKILDFMK 180  
QY 181 DVMTKLSTYSYQFAAVQFSTSYKTEFDFSDYVKRDPALLKRVKMLLNTTFGAINYV 240  
DB 181 DVMTKLSTYSYQFAAVQFSTSYKTEFDFSDYVKRDPALLKRVKMLLNTTFGAINYV 240  
QY 241 ATEVREBELGARPDATKYLIIITTOEATDNGNIDAKOIIYIIIGIGHFQTKESQETLH 300  
DB 241 ATEVREBELGARPDATKYLIIITTOEATDNGNIDAKOIIYIIIGIGHFQTKESQETLH 300  
QY 301 KFAASKPASEFYKIIDTFEKLKDLFTLQKTIYIEGTSKODLTFNMELSSGISADLSR 360  
DB 301 KFAASKPASEFYKIIDTFEKLKDLFTLQKTIYIEGTSKODLTFNMELSSGISADLSR 360  
QY 361 GHAAVGAAGADWAGGFLDLKADLDDTFIIGNEPLTFPEVRAGYLYGYVWMLPSRQKISL 420  
DB 361 GHAAVGAAGADWAGGFLDLKADLDDTFIIGNEPLTFPEVRAGYLYGYVWMLPSRQKISL 420  
QY 421 ASGARVYQHMGRVLLFOEPQGGHMSVOYTHGNOIGSYFGGELGQVVDODGTELLLI 480  
DB 421 ASGARVYQHMGRVLLFOEPQGGHMSVOYTHGNOIGSYFGGELGQVVDODGTELLLI 480  
QY 481 GAPLFYGGORGGRVFIYORROLGFEFEVSELQDPPGYLGRFCEATLALTDINGDLVVA 540  
DB 481 GAPLFYGGORGGRVFIYORROLGFEFEVSELQDPPGYLGRFCEATLALTDINGDLVVA 540  
QY 541 VGAPLEEGAAVYIFNGRHGGLSPQPSQRIEGTVLSGIQWFGRSIHGVKDLBGDGLADVA 600  
DB 541 VGAPLEEGAAVYIFNGRHGGLSPQPSQRIEGTVLSGIQWFGRSIHGVKDLBGDGLADVA 600

DB 541 VGAPLEEGAAVYIFNGRHGGLSPQPSQRIEGTVLSGIQWFGRSIHGVKDLBGDGLADVA 600  
QY 601 VGASQMIIVLSSRPVVMYTLMSFSPAEIPVHEVECSYTSNMKESVNTTICFOIKSLY 660  
DB 601 VGASQMIIVLSSRPVVMYTLMSFSPAEIPVHEVECSYTSNMKESVNTTICFOIKSLY 660  
QY 661 POFQGRVANIYTLTQDGHRTTRRGFLPGGRHRLRNIAVTTSMSCTDPSFHPVVCOD 720  
DB 661 POFQGRVANIYTLTQDGHRTTRRGFLPGGRHRLRNIAVTTSMSCTDPSFHPVVCOD 720  
QY 721 LISFINVSLNPSLMEEGTFRDQAGKDIPIILRPSLSEETWEIPEPKKCGEDKCEAN 780  
DB 721 LISFINVSLNPSLMEEGTFRDQAGKDIPIILRPSLSEETWEIPEPKKCGEDKCEAN 780  
QY 781 LRVSFSPARRALRLTFASTLVELSISNLEBAYWQDLHPPGISFPKVMKPKHSQ 840  
DB 781 LRVSFSPARRALRLTFASTLVELSISNLEBAYWQDLHPPGISFPKVMKPKHSQ 840  
QY 841 IPVSCEBLPESRRLSLRALSQNVSSPIFKAGHSVALQMMFNTLVNSGDSVEIHANVTC 900  
DB 841 IPVSCEBLPESRRLSLRALSQNVSSPIFKAGHSVALQMMFNTLVNSGDSVEIHANVTC 900  
QY 901 NNEDSDLEEDNSATTTIPIIYPINILIQDQDSTLYSFTPKGPKIHQVGMTOVRIOPS 960  
DB 901 NNEDSDLEEDNSATTTIPIIYPINILIQDQDSTLYSFTPKGPKIHQVGMTOVRIOPS 960  
QY 961 IHDNITPLEAVYGVPOPSRGPITTHQWSVQMPVPCHEDELRDLPAEPCLPALFR 1020  
DB 961 IHDNITPLEAVYGVPOPSRGPITTHQWSVQMPVPCHEDELRDLPAEPCLPALFR 1020  
QY 1021 CPVVFROEIIIVQVIGTLELVBGEIASSMFSLSISLISFNSSKHFLYGSNASLAQVVK 1080  
DB 1021 CPVVFROEIIIVQVIGTLELVBGEIASSMFSLSISLISFNSSKHFLYGSNASLAQVVK 1080  
QY 1081 VDVYTERQMTLYLYLSGIGLLLLIFLYLYKVPFKRNLKEXMEAGRGVPGNIPAEBS 1140  
DB 1081 VDVYTERQMTLYLYLSGIGLLLLIFLYLYKVPFKRNLKEXMEAGRGVPGNIPAEBS 1140  
QY 1141 EQLASQEGADPGCLKPLHEKDSRSGGKD 1170  
DB 1141 EQLASQEGADPGCLKPLHEKDSRSGGKD 1170

RESULT 5  
US-10-473-127-1739  
; Sequence 1739, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1739  
; LENGTH: 1170  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1739

Query Match 99.9%; Score 6098; DB 16; Length 1170;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKDSCITVMAWALLSGFFFPAPASSYNLDVNGARSPSPRAGRHFGRVLDVNGVIVGA 60  
 DB 1 MKDSCITVMAWALLSGFFFPAPASSYNLDVNGARSPSPRAGRHFGRVLDVNGVIVGA 60  
 QY 61 PGEKSTGSLVYCCSGTGCHCLPVTLRGNTSKYLGMTLATDPTDGSILACDPSLRTCD 120  
 DB 61 PGEKSTGSLVYCCSGTGCHCLPVTLRGNTSKYLGMTLATDPTDGSILACDPSLRTCD 120  
 QY 121 QNTYLSGLCYLFRONLQGPMLQGRPGFQECIKGNVDLVFLFDGSMSLQPDFQKILDFMK 180  
 DB 121 QNTYLSGLCYLFRONLQGPMLQGRPGFQECIKGNVDLVFLFDGSMSLQPDFQKILDFMK 180  
 QY 181 DVMKLSTNTSYQFAAVOSTSYKTEFSDVYKRDPAALLKHVGHMLLTNTFGAINVY 240  
 DB 181 DVMKLSTNTSYQFAAVOSTSYKTEFSDVYKRDPAALLKHVGHMLLTNTFGAINVY 240  
 QY 241 ATEVREBELGARPDATKVLIIITDGEATDSGNIDAADIIIRYIIGIGHFQTKESQETLH 300  
 DB 241 ATEVREBELGARPDATKVLIIITDGEATDSGNIDAADIIIRYIIGIGHFQTKESQETLH 300  
 QY 301 KPASKPASEFVKILDTPEKLDLFTLEOKIYVIEGTSKODLTSFNMELSSGSIADLSR 360  
 DB 301 KPASKPASEFVKILDTPEKLDLFTLEOKIYVIEGTSKODLTSFNMELSSGSIADLSR 360  
 QY 361 GHAVVAGAKDMAGFLDLKADLDDPTFIGNEPLEPEVRAGYLGVTYTWLPSRKTSLL 420  
 DB 361 GHAVVAGAKDMAGFLDLKADLDDPTFIGNEPLEPEVRAGYLGVTYTWLPSRKTSLL 420  
 QY 421 ASGAPRYOHMGVILLFOEPQGGHMSQVQTHGTIGSYFGGELCGVDVDDGKTELLLI 480  
 DB 421 ASGAPRYOHMGVILLFOEPQGGHMSQVQTHGTIGSYFGGELCGVDVDDGKTELLLI 480  
 QY 481 GAPLFYGGORGRVITYQRRLQGFEEVSELQDPEYPLGRFEBATLTALTDINGDGLVYA 540  
 DB 481 GAPLFYGGORGRVITYQRRLQGFEEVSELQDPEYPLGRFEBATLTALTDINGDGLVYA 540  
 QY 541 VGAPLEEGAGVYIFNGRHGSLSPQSORLBTQVLSGIQWFGSRHGVYLEDGDLADVA 600  
 DB 541 VGAPLEEGAGVYIFNGRHGSLSPQSORLBTQVLSGIQWFGSRHGVYLEDGDLADVA 600  
 QY 601 VGASQOMLVLSRPVVDWVTLMSFSPAIPVHEVCSYSTSNKMEGVNITTCFOIKSLY 660  
 DB 601 VGASQOMLVLSRPVVDWVTLMSFSPAIPVHEVCSYSTSNKMEGVNITTCFOIKSLY 660  
 QY 661 POFQGRLVANLTYTQLDGHRTTRRGGLPFGGRHBLRRNIAVTTSMSCDPSFHFVPCVD 720  
 DB 661 POFQGRLVANLTYTQLDGHRTTRRGGLPFGGRHBLRRNIAVTTSMSCDPSFHFVPCVD 720  
 QY 721 LIISPINVSINFLSMBEEGPRDORAQKDIPLILASLHSETWEIPEFKNCEEDKKCAN 780  
 DB 721 LIISPINVSINFLSMBEEGPRDORAQKDIPLILASLHSETWEIPEFKNCEEDKKCAN 780  
 QY 781 LRVSPSPARSRLRLTAFASSLVELSLNLEBDAYVOLDLHFPGLSFRKYMELKPSHQ 840  
 DB 781 LRVSPSPARSRLRLTAFASSLVELSLNLEBDAYVOLDLHFPGLSFRKYMELKPSHQ 840  
 QY 841 LPVSEEBELPESRRLSLRASCNVSPIFKAGHVALQWMMFNTLVNMSGDSVELHANTYC 900  
 DB 841 LPVSEEBELPESRRLSLRASCNVSPIFKAGHVALQWMMFNTLVNMSGDSVELHANTYC 900  
 QY 901 NNBDLJEDNSATIIIPILYPINLIDQEDSTLYVSTPKPIHVKHMYOYRIOPS 960  
 DB 901 NNBDLJEDNSATIIIPILYPINLIDQEDSTLYVSTPKPIHVKHMYOYRIOPS 960  
 QY 961 IHDHNIPTLEAVVGPQPSSEGPITHQMSVQMBPVPCYEDLEJLPPAAEBCPLGALFR 1020  
 DB 961 IHDHNIPTLEAVVGPQPSSEGPITHQMSVQMBPVPCYEDLEJLPPAAEBCPLGALFR 1020  
 QY 1021 CPVVRQELIVQVIGTLELVEIEASSMFSLCSSLISFNSKHHLXGNSASLAQVYMK 1080

DB 1021 CPVVRQELIVQVIGTLELVEIEASSMFSLCSSLISFNSKHHLXGNSASLAQVYMK 1080  
 QY 1081 DVVYERKOMLYLYLSGIGLLLLLIPIVLVYKGFGRNLIKERKEAGRGVPNGIPADS 1140  
 DB 1081 DVVYERKOMLYLYLSGIGLLLLLIPIVLVYKGFGRNLIKERKEAGRGVPNGIPADS 1140  
 QY 1141 EQLASQDAGDPGCLKPLHEKDSGSGGKD 1170  
 DB 1141 EQLASQDAGDPGCLKPLHEKDSGSGGKD 1170

RESULT 6  
 US-10-473-127-1742  
 ; Sequence 1742, Application US/10473127  
 ; Publication No. US20040236091A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Zycos Inc.  
 ; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
 ; FILE REFERENCE: 08191-026W01  
 ; CURRENT APPLICATION NUMBER: US/10/473,127  
 ; PRIOR FILING DATE: 2003-09-26  
 ; PRIOR APPLICATION NUMBER: 60/279,495  
 ; PRIOR FILING DATE: 2001-03-28  
 ; PRIOR APPLICATION NUMBER: 60/292,544  
 ; PRIOR FILING DATE: 2001-05-21  
 ; PRIOR APPLICATION NUMBER: 60/310,801  
 ; PRIOR FILING DATE: 2001-08-08  
 ; PRIOR APPLICATION NUMBER: 60/326,370  
 ; PRIOR FILING DATE: 2001-10-01  
 ; PRIOR APPLICATION NUMBER: 60/336,780  
 ; PRIOR FILING DATE: 2001-12-04  
 ; PRIOR APPLICATION NUMBER: 60/358,985  
 ; PRIOR FILING DATE: 2002-02-20  
 ; NUMBER OF SEQ ID NOS: 2041  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1742  
 ; LENGTH: 1170  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-473-127-1742

Query Match 99.9%; Score 6098; DB 16; Length 1170;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKDSCITVMAWALLSGFFFPAPASSYNLDVNGARSPSPRAGRHFGRVLDVNGVIVGA 60  
 DB 1 MKDSCITVMAWALLSGFFFPAPASSYNLDVNGARSPSPRAGRHFGRVLDVNGVIVGA 60  
 QY 61 PGEKSTGSLVYCCSGTGCHCLPVTLRGNTSKYLGMTLATDPTDGSILACDPSLRTCD 120  
 DB 61 PGEKSTGSLVYCCSGTGCHCLPVTLRGNTSKYLGMTLATDPTDGSILACDPSLRTCD 120  
 QY 121 QNTYLSGLCYLFRONLQGPMLQGRPGFQECIKGNVDLVFLFDGSMSLQPDFQKILDFMK 180  
 DB 121 QNTYLSGLCYLFRONLQGPMLQGRPGFQECIKGNVDLVFLFDGSMSLQPDFQKILDFMK 180  
 QY 181 DVMKLSTNTSYQFAAVOSTSYKTEFSDVYKRDPAALLKHVGHMLLTNTFGAINVY 240  
 DB 181 DVMKLSTNTSYQFAAVOSTSYKTEFSDVYKRDPAALLKHVGHMLLTNTFGAINVY 240  
 QY 241 ATEVREBELGARPDATKVLIIITDGEATDSGNIDAADIIIRYIIGIGHFQTKESQETLH 300  
 DB 241 ATEVREBELGARPDATKVLIIITDGEATDSGNIDAADIIIRYIIGIGHFQTKESQETLH 300  
 QY 301 KPASKPASEFVKILDTPEKLDLFTLEOKIYVIEGTSKODLTSFNMELSSGSIADLSR 360  
 DB 301 KPASKPASEFVKILDTPEKLDLFTLEOKIYVIEGTSKODLTSFNMELSSGSIADLSR 360  
 QY 361 GHAVVAGAKDMAGFLDLKADLDDPTFIGNEPLEPEVRAGYLGVTYTWLPSRKTSLL 420  
 DB 361 GHAVVAGAKDMAGFLDLKADLDDPTFIGNEPLEPEVRAGYLGVTYTWLPSRKTSLL 420

QY 421 ASGARPYOHMGRVLLFOEPQGGHMSQVQTHGTQISYFGGELCGVVDODGETELLII 480  
DB 421 ASGARPYOHMGRVLLFOEPQGGHMSQVQTHGTQISYFGGELCGVVDODGETELLII 480  
QY 481 GAPLFYEGORGRVFIYORRQLGFEVESELQCDPGYVGRGFEAITALTIDINGDLVVA 540  
DB 481 GAPLFYEGORGRVFIYORRQLGFEVESELQCDPGYVGRGFEAITALTIDINGDLVVA 540  
QY 541 VGAPLEEGGAVYIFNGRHGGLSPQSORIBGTQVLSGIOMFGRSHGVKDEGGDLAVA 600  
DB 541 VGAPLEEGGAVYIFNGRHGGLSPQSORIBGTQVLSGIOMFGRSHGVKDEGGDLAVA 600  
QY 601 VGASQMTVLSRPVVDVMTLMSFSPAEIPVHEVCSTYSNMKEGVNITICFOIKSLY 660  
DB 601 VGASQMTVLSRPVVDVMTLMSFSPAEIPVHEVCSTYSNMKEGVNITICFOIKSLY 660  
QY 661 POFQGRLVANLTYTLQDGHRTTRRGLFPGGRHRLRNIAVTTSMSCDTSFHFVVCVD 720  
DB 661 POFQGRLVANLTYTLQDGHRTTRRGLFPGGRHRLRNIAVTTSMSCDTSFHFVVCVD 720  
QY 721 LISPINVSLNFSLMEEGTTPRDQAOQKDIPIILRPSLHSETWEIPFEKNGCEDKKEAN 780  
DB 721 LISPINVSLNFSLMEEGTTPRDQAOQKDIPIILRPSLHSETWEIPFEKNGCEDKKEAN 780  
QY 781 LRVSPSPARSRLRLTAFASLSVELSLSNLEBDAYWQDLHFPGLSFRKVEMLKPHSQ 840  
DB 781 LRVSPSPARSRLRLTAFASLSVELSLSNLEBDAYWQDLHFPGLSFRKVEMLKPHSQ 840  
QY 841 IPVSCEELPESRRLSLRALSQVSSPIFKAGSHVALQMMFNTLVNSMGDSVELHANVC 900  
DB 841 IPVSCEELPESRRLSLRALSQVSSPIFKAGSHVALQMMFNTLVNSMGDSVELHANVC 900  
QY 901 NNEBSDLIEDNSATITIIPIILPINLIDQEDSTLYSFTPKGPIHVKMYOVRIOPS 960  
DB 901 NNEBSDLIEDNSATITIIPIILPINLIDQEDSTLYSFTPKGPIHVKMYOVRIOPS 960  
QY 961 IHDNHIPTLEAVGVPOPSBGPITHQMSVOMEPPVPCHEDELERLDAAPCPLGALFR 1020  
DB 961 IHDNHIPTLEAVGVPOPSBGPITHQMSVOMEPPVPCHEDELERLDAAPCPLGALFR 1020  
QY 1021 CPVVRQEBILVQVIGTLELVEIEASSMFSLSISIFNSKHFHLVGSNASLAQVVMK 1080  
DB 1021 CPVVRQEBILVQVIGTLELVEIEASSMFSLSISIFNSKHFHLVGSNASLAQVVMK 1080  
QY 1081 DVVVEKQMLTYLVSIGLILLLIFLYLYKVGFPFRNLKEKMEAGRGVDPNGIPADS 1140  
DB 1081 DVVVEKQMLTYLVSIGLILLLIFLYLYKVGFPFRNLKEKMEAGRGVDPNGIPADS 1140  
QY 1141 EQLASGOEAGDPGCLKPLHEKDSGGKXD 1170  
DB 1141 EQLASGOEAGDPGCLKPLHEKDSGGKXD 1170

RESULT 7  
US-10-741-600-1088  
; Sequence 1088, Application US/10741600  
; Publication No. US20050026169A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; FILE REFERENCE: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF  
; CURRENT FILING DATE: 2003-12-22  
; NUMBER OF SEQ ID NOS: 7397  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1088  
; LENGTH: 1170  
; TYPE: PRF  
; ORGANISM: Homo sapiens  
US-10-741-600-1088

Query Match 99.9%; Score 6098; DB 17; Length 1170;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MKDSCITVMMALLSGFFFPAPASSTYLDVYRGARSFSPPAAGHRFGYRVYQVNGVYVGA 60  
DB 1 MKDSCITVMMALLSGFFFPAPASSTYLDVYRGARSFSPPAAGHRFGYRVYQVNGVYVGA 60  
QY 61 PGEAGNSTGSLYQCCSGTGHCIPVTLRGSNTYSKILGNTLTDPDGSIIACDPGLSRTCD 120  
DB 61 PGEAGNSTGSLYQCCSGTGHCIPVTLRGSNTYSKILGNTLTDPDGSIIACDPGLSRTCD 120  
QY 121 QNTYLSGLCYLFRQNLQGPMLQGRPGFOECIKGNVDLVFLFDGSMSLQDPEFOKILDFMK 180  
DB 121 QNTYLSGLCYLFRQNLQGPMLQGRPGFOECIKGNVDLVFLFDGSMSLQDPEFOKILDFMK 180  
QY 181 DVMKGLSNTSYQFAAVOPSTSYKTEEPFSDYVVRKDPDALLKRYKMLLTNTFGAINTY 240  
DB 181 DVMKGLSNTSYQFAAVOPSTSYKTEEPFSDYVVRKDPDALLKRYKMLLTNTFGAINTY 240  
QY 241 ATEVFRBELGARPATKYLLIITDGEATDSGNIDPAKDIIRYIIGIKHFQTKESQETLH 300  
DB 241 ATEVFRBELGARPATKYLLIITDGEATDSGNIDPAKDIIRYIIGIKHFQTKESQETLH 300  
QY 301 KFASKPASEFYKILDTBEKLDLFTTELQKKIYYIEGTSKODLISFNNELSSSGISADLSR 360  
DB 301 KFASKPASEFYKILDTBEKLDLFTTELQKKIYYIEGTSKODLISFNNELSSSGISADLSR 360  
QY 361 GHAVVAVGAKDWAAGSLDLKADLQDDPTFIGNELTEVAVAGLYGVYVWLPBQKQSL 420  
DB 361 GHAVVAVGAKDWAAGSLDLKADLQDDPTFIGNELTEVAVAGLYGVYVWLPBQKQSL 420  
QY 421 ASGARPYOHMGRVLLFOEPQGGHMSQVQTHGTQISYFGGELCGVVDODGETELLII 480  
DB 421 ASGARPYOHMGRVLLFOEPQGGHMSQVQTHGTQISYFGGELCGVVDODGETELLII 480  
QY 481 GAPLFYEGORGRVFIYORRQLGFEVESELQCDPGYVGRGFEAITALTIDINGDLVVA 540  
DB 481 GAPLFYEGORGRVFIYORRQLGFEVESELQCDPGYVGRGFEAITALTIDINGDLVVA 540  
QY 541 VGAPLEEGGAVYIFNGRHGGLSPQSORIBGTQVLSGIOMFGRSHGVKDEGGDLAVA 600  
DB 541 VGAPLEEGGAVYIFNGRHGGLSPQSORIBGTQVLSGIOMFGRSHGVKDEGGDLAVA 600  
QY 601 VGASQMTVLSRPVVDVMTLMSFSPAEIPVHEVCSTYSNMKEGVNITICFOIKSLY 660  
DB 601 VGASQMTVLSRPVVDVMTLMSFSPAEIPVHEVCSTYSNMKEGVNITICFOIKSLY 660  
QY 661 POFQGRLVANLTYTLQDGHRTTRRGLFPGGRHRLRNIAVTTSMSCDTSFHFVVCVD 720  
DB 661 POFQGRLVANLTYTLQDGHRTTRRGLFPGGRHRLRNIAVTTSMSCDTSFHFVVCVD 720  
QY 721 LISPINVSLNFSLMEEGTTPRDQAOQKDIPIILRPSLHSETWEIPFEKNGCEDKKEAN 780  
DB 721 LISPINVSLNFSLMEEGTTPRDQAOQKDIPIILRPSLHSETWEIPFEKNGCEDKKEAN 780  
QY 781 LRVSPSPARSRLRLTAFASLSVELSLSNLEBDAYWQDLHFPGLSFRKVEMLKPHSQ 840  
DB 781 LRVSPSPARSRLRLTAFASLSVELSLSNLEBDAYWQDLHFPGLSFRKVEMLKPHSQ 840  
QY 841 IPVSCEELPESRRLSLRALSQVSSPIFKAGSHVALQMMFNTLVNSMGDSVELHANVC 900  
DB 841 IPVSCEELPESRRLSLRALSQVSSPIFKAGSHVALQMMFNTLVNSMGDSVELHANVC 900  
QY 901 NNEBSDLIEDNSATITIIPIILPINLIDQEDSTLYSFTPKGPIHVKMYOVRIOPS 960  
DB 901 NNEBSDLIEDNSATITIIPIILPINLIDQEDSTLYSFTPKGPIHVKMYOVRIOPS 960  
QY 961 IHDNHIPTLEAVGVPOPSBGPITHQMSVOMEPPVPCHEDELERLDAAPCPLGALFR 1020  
DB 961 IHDNHIPTLEAVGVPOPSBGPITHQMSVOMEPPVPCHEDELERLDAAPCPLGALFR 1020  
QY 1021 CPVVRQEBILVQVIGTLELVEIEASSMFSLSISIFNSKHFHLVGSNASLAQVVMK 1080



```

Db      1021  CQVVERQELVQVIGTLELVEGEIEASMSFSCSSISISFNKHHLYGSNASTLAQVYMK 1080
Qy      1081  VDVTYRKQMLYLYLSGIGGLLLLIPIVLYKVGFFKRNLEKKEAGRGVNGI PAEDS 1140
Db      1081  VDVTYRKQMLYLYLSGIGGLLLLIPIVLYKVGFFKRNLEKKEAGRGVNGI PAEDS 1140
Qy      1141  EQLASGQAGDPCCKPLHEKDESGGGKD 1170
Db      1141  EQLASGQAGDPCCKPLHEKDESGGGKD 1170

RESULT 8
US-11-062-290-1
; Sequence 1, Application US/11062290
; Publication No. US20050142134A1
; GENERAL INFORMATION:
; APPLICANT: KAPUSTAY, PAMELA M.
; APPLICANT: LEWIS, REX H.
; TITLE OF INVENTION: LFA-1 ALPHA SUBUNIT ANTIBODIES AND METHODS OF USE
; FILE REFERENCE: 046007/0272304
; CURRENT APPLICATION NUMBER: US/11/062,290
; PRIOR FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: US/10/261,164
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-062-290-1

Query Match      99.9%; Score 6098; DB 20; Length 1170;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1      MKDSCITWAMALLSGFFFPAPASSYNLDVGRASFSPPRAGRHFGRVLYQVNGVIVGA 60
Db      1      MKDSCITWAMALLSGFFFPAPASSYNLDVGRASFSPPRAGRHFGRVLYQVNGVIVGA 60
Qy      61      PGBGNSGSLVYQCSGCTGHCPLVTLRGSNTYSKYLGMTLATDPTDGSILACDPSLRCTD 120
Db      61      PGBGNSGSLVYQCSGCTGHCPLVTLRGSNTYSKYLGMTLATDPTDGSILACDPSLRCTD 120
Qy      121     QNTYLSGLCYLFRQMLQCPMLQGRPGFOECIKGNVDLVELPFGSMSLOPDEFOKILDFMK 180
Db      121     QNTYLSGLCYLFRQMLQCPMLQGRPGFOECIKGNVDLVELPFGSMSLOPDEFOKILDFMK 180
Qy      181     DVNKKLSNTSYQFAAVQSTSYKTEFDSYVKKRDPALLKRVKMLLTNTFGAINVY 240
Db      181     DVNKKLSNTSYQFAAVQSTSYKTEFDSYVKKRDPALLKRVKMLLTNTFGAINVY 240
Qy      241     ATTVREBELGARPDATKVLIIITDEBANDSGNIDAAKDIIRITIGIGKHFQKESQETLH 300
Db      241     ATTVREBELGARPDATKVLIIITDEBANDSGNIDAAKDIIRITIGIGKHFQKESQETLH 300
Qy      301     KFASPKASBFVKILTFEKLKDLFTELQKIYVIGSTSKODLTFPMELSSSGISADLSR 360
Db      301     KFASPKASBFVKILTFEKLKDLFTELQKIYVIGSTSKODLTFPMELSSSGISADLSR 360
Qy      361     GHAVVGAAGAKMAGGFLDLKADLDDFTFIGNBPLTPVRAGYLYTVTWLPSRKTSLL 420
Db      361     GHAVVGAAGAKMAGGFLDLKADLDDFTFIGNBPLTPVRAGYLYTVTWLPSRKTSLL 420
Qy      421     ASGARRYQMGKRVLLFOEPQGGGHSQVQTHGTQISYFGBELGCVVDODGRTLELLI 480
Db      421     ASGARRYQMGKRVLLFOEPQGGGHSQVQTHGTQISYFGBELGCVVDODGRTLELLI 480
Qy      481     GAPLFYGEORGRGVETLYQRRLGFEEVSELODPPGLGRFGEAITALTLDINGDGLVYA 540
Db      481     GAPLFYGEORGRGVETLYQRRLGFEEVSELODPPGLGRFGEAITALTLDINGDGLVYA 540

```

```

Qy      541     VGAPLEBQAGYVIFNGRHGSLPSPOSORIEGNOVLSGIQWFGRSIHGYKDLBGDLADVA 600
Db      541     VGAPLEBQAGYVIFNGRHGSLPSPOSORIEGNOVLSGIQWFGRSIHGYKDLBGDLADVA 600
Qy      601     VGASOMIVLSSRPVMDVMTLMSFSPAIEPVHEVECSYSTSNKKEGVNITICFOIKSLY 660
Db      601     VGASOMIVLSSRPVMDVMTLMSFSPAIEPVHEVECSYSTSNKKEGVNITICFOIKSLY 660
Qy      661     POFQGRVLANITTYLQDLGHRTRRRGLFPGGRHLEKRNIAVTTSMCTDSFHHFVYQD 720
Db      661     POFQGRVLANITTYLQDLGHRTRRRGLFPGGRHLEKRNIAVTTSMCTDSFHHFVYQD 720
Qy      721     LISPIVNSLNSWEEBCTPRDQAGKDIPILLPSLSHSTWELPEKNGGEODKGRAN 780
Db      721     LISPIVNSLNSWEEBCTPRDQAGKDIPILLPSLSHSTWELPEKNGGEODKGRAN 780
Qy      781     LRVSPSPASRLRLTAPASLSVELSLNEEDAWYQDLHFPGLSFRKYMELKPSHQ 840
Db      781     LRVSPSPASRLRLTAPASLSVELSLNEEDAWYQDLHFPGLSFRKYMELKPSHQ 840
Qy      841     IPVSCBELPEBSRLLSRALSCNVSSPIFKAGHSVALQMMFNTLVNSNGDSVELHANVTC 900
Db      841     IPVSCBELPEBSRLLSRALSCNVSSPIFKAGHSVALQMMFNTLVNSNGDSVELHANVTC 900
Qy      901     NNEDSDLEDNSATTIIPILYPINILIODQDSTLYSFTKGPRIHOVKMYQVRIOPS 960
Db      901     NNEDSDLEDNSATTIIPILYPINILIODQDSTLYSFTKGPRIHOVKMYQVRIOPS 960
Qy      961     IHDNIPTLEAVGPOPSPSGPITTHQMSVOMEPVPCHYEDLERLPPAAEPCLGALFR 1020
Db      961     IHDNIPTLEAVGPOPSPSGPITTHQMSVOMEPVPCHYEDLERLPPAAEPCLGALFR 1020
Qy      1021    CPVYFROELIVQVIGTLELVEGEIEASMSFSCSSISISFNKHHLYGSNASTLAQVYMK 1080
Db      1021    CPVYFROELIVQVIGTLELVEGEIEASMSFSCSSISISFNKHHLYGSNASTLAQVYMK 1080
Qy      1081    VDVTYRKQMLYLYLSGIGGLLLLIPIVLYKVGFFKRNLEKKEAGRGVNGI PAEDS 1140
Db      1081    VDVTYRKQMLYLYLSGIGGLLLLIPIVLYKVGFFKRNLEKKEAGRGVNGI PAEDS 1140
Qy      1141    EQLASGQAGDPCCKPLHEKDESGGGKD 1170
Db      1141    EQLASGQAGDPCCKPLHEKDESGGGKD 1170

RESULT 9
US-10-741-600-1086
; Sequence 1086, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CLO01499
; CURRENT APPLICATION NUMBER: US/10/741,600
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1086
; LENGTH: 1223
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-1086

Query Match      99.3%; Score 6061.5; DB 17; Length 1223;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 1169; Conservative 0; Mismatches 1; Indels 53; Gaps 1;

Qy      1      MKDSCITWAMALLSGFFFPAPASSYNLDVGRASFSPPRAGRHFGRVLYQVNGVIVGA 60
Db      1      MKDSCITWAMALLSGFFFPAPASSYNLDVGRASFSPPRAGRHFGRVLYQVNGVIVGA 60
Qy      61      PGBGNSGSLVYQCSGCTGHCPLVTLRGSNTYSKYLGMTLATDPTDGSILACDPSLRCTD 120

```

```

Db      61  PGEAGSTSLYQCSGTHCLPVTLRGNSNTSKYLGMTLATDPTDGSILACDPGLSRTCD 120
Qy      121  QNTYLSGICYLFRONLQGRPGROECIKGNVDVLFPLDGSMSLOPDEFQKILDFMK 180
Db      121  QNTYLSGICYLFRONLQGRPGROECIKGNVDVLFPLDGSMSLOPDEFQKILDFMK 180
Qy      181  DVMKLSNTSYQFAAVQSTSYKTEPDSYVKRDPALLKHYKHMILLNTFGAINVY 240
Db      181  DVMKLSNTSYQFAAVQSTSYKTEPDSYVKRDPALLKHYKHMILLNTFGAINVY 240
Qy      241  ATEVFEELGARPDATKVLIIITDGEATDSGNIDAADIIIRYIIIGIKHFQTKESQETLH 300
Db      241  ATEVFEELGARPDATKVLIIITDGEATDSGNIDAADIIIRYIIIGIKHFQTKESQETLH 300
Qy      301  KFAKSPASEPVKILDTPEKLDLFTTELQKTIYVIEGTSKODLTSPNMELSSSGISADLSR 360
Db      301  KFAKSPASEPVKILDTPEKLDLFTTELQKTIYVIEGTSKODLTSPNMELSSSGISADLSR 360
Qy      361  GHAVVAGAVGAKDMAGFLDLKADLQDDTFIGNEBLTPBEVAGYLGIVTWMPSROKTSLL 420
Db      361  GHAVVAGAVGAKDMAGFLDLKADLQDDTFIGNEBLTPBEVAGYLGIVTWMPSROKTSLL 420
Qy      421  ASGAPRYQHMGRVILLFQEPQGGHWSQVQTIHGQISYFGGELCGVDVDQGETELLII 480
Db      421  ASGAPRYQHMGRVILLFQEPQGGHWSQVQTIHGQISYFGGELCGVDVDQGETELLII 480
Qy      481  GAPLFYGEORGRVITYORROLGFEVSELOQDPGYPLGRFGEALTALTDINGGLADVA 540
Db      481  GAPLFYGEORGRVITYORROLGFEVSELOQDPGYPLGRFGEALTALTDINGGLADVA 540
Qy      541  VGAPLEBOGAVYIFNGRHGGLSPQSPQRIEGTQVLSGIQWFGRSIHGVKLEBGDLADVA 600
Db      541  VGAPLEBOGAVYIFNGRHGGLSPQSPQRIEGTQVLSGIQWFGRSIHGVKLEBGDLADVA 600
Qy      601  VGASQMTVLSRPAVDWMTLMSFSPAIPIVHEVCSYSTSNKMEGVNITICFOIKSLY 660
Db      601  VGASQMTVLSRPAVDWMTLMSFSPAIPIVHEVCSYSTSNKMEGVNITICFOIKSLY 660
Qy      661  POFQRLVANTLYTLQLDGHRTRRGCLFPGRHETRLNIATWTSMSCTDPSFHPVCOD 720
Db      661  POFQRLVANTLYTLQLDGHRTRRGCLFPGRHETRLNIATWTSMSCTDPSFHPVCOD 720
Qy      721  LISPIVNSLNSLWEEBGTPRDQRAQKODIPILRPSLHSETWLPPEKNGCEDKCKCAN 780
Db      721  LISPIVNSLNSLWEEBGTPRDQRAQKODIPILRPSLHSETWLPPEKNGCEDKCKCAN 780
Qy      781  LRVFSPPARSALRLTAFASLSVELSLNLEEDAYVQDLHFPFGLSFRKVENMLKPSHQ 840
Db      781  LRVFSPPARSALRLTAFASLSVELSLNLEEDAYVQDLHFPFGLSFRKVENMLKPSHQ 840
Qy      841  IPVGEELPERSRLSLALSCVSPPIKAGHSVALQWMTLTVNSSGDSVELHANVTC 900
Db      841  IPVGEELPERSRLSLALSCVSPPIKAGHSVALQWMTLTVNSSGDSVELHANVTC 900
Qy      901  NNEBSDLLEDSATYIPIILYPINLLIOEDOSTLYSFTPKGPIKHVKNHYQ----- 954
Db      901  NNEBSDLLEDSATYIPIILYPINLLIOEDOSTLYSFTPKGPIKHVKNHYQ----- 954
Qy      955  -----VRIQPSIHNIHNP 967
Db      961  EMQTSKQILCRPADAEHTVGAQEBELPCPMGVSEAPRDNIRAGPCRVRIQPSIHNIHNP 1020
Qy      968  TLEAVVGPORPSEBPIITHQWSVQMEPRVPCHELELRLPDAABCLFGALFRCPVVRQ 1027
Db      1021  TLEAVVGPORPSEBPIITHQWSVQMEPRVPCHELELRLPDAABCLFGALFRCPVVRQ 1080
Qy      1028  EILVQVIGTLELVEIRBASMPSLCSSLSISFNSKHFHLVGSNSLSLQVVMKDVVYEX 1087
Db      1081  EILVQVIGTLELVEIRBASMPSLCSSLSISFNSKHFHLVGSNSLSLQVVMKDVVYEX 1140
Qy      1088  QMLYLYVLSGIGILLLLIFLYVKVGFPRKMLKEKMEAGRGVNGIPADBSQLASGQ 1147

```

```

Db      1141  QMLYLYVLSGIGILLLLIFLYVKVGFPRKMLKEKMEAGRGVNGIPADBSQLASGQ 1200
Qy      1148  EAGDPGLKPLHEKDSRSGGKD 1170
Db      1201  EAGDPGLKPLHEKDSRSGGKD 1223

RESULT 10
US-10-408-765A-295
; Sequence 295, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Faby, Bojn D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Marnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408.765A
; NUMBER OF INVENTION: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 295
; LENGTH: 1223
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-295

Query Match      99.1%; Score 6053.5; DB 16; Length 1223;
Beet Local Similarity 95.5%; Pred. No. 0;
Matches 1168; Conservative 0; Mismatches 2; Indels 53; Gaps 1;

Qy      1  MKOSCTVMMAMALSGFFPAPASSYMLDVRGARSFSPRAGRHFGYRLVQVNGVIVGA 60
Db      1  MKOSCTVMMAMALSGFFPAPASSYMLDVRGARSFSPRAGRHFGYRLVQVNGVIVGA 60
Qy      61  PGEAGSTSLYQCSGTHCLPVTLRGNSNTSKYLGMTLATDPTDGSILACDPGLSRTCD 120
Db      61  PGEAGSTSLYQCSGTHCLPVTLRGNSNTSKYLGMTLATDPTDGSILACDPGLSRTCD 120
Qy      121  QNTYLSGICYLFRONLQGRPGROECIKGNVDVLFPLDGSMSLOPDEFQKILDFMK 180
Db      121  QNTYLSGICYLFRONLQGRPGROECIKGNVDVLFPLDGSMSLOPDEFQKILDFMK 180
Qy      181  DVMKLSNTSYQFAAVQSTSYKTEPDSYVKRDPALLKHYKHMILLNTFGAINVY 240
Db      181  DVMKLSNTSYQFAAVQSTSYKTEPDSYVKRDPALLKHYKHMILLNTFGAINVY 240
Qy      241  ATEVFEELGARPDATKVLIIITDGEATDSGNIDAADIIIRYIIIGIKHFQTKESQETLH 300
Db      241  ATEVFEELGARPDATKVLIIITDGEATDSGNIDAADIIIRYIIIGIKHFQTKESQETLH 300
Qy      301  KFAKSPASEPVKILDTPEKLDLFTTELQKTIYVIEGTSKODLTSPNMELSSSGISADLSR 360
Db      301  KFAKSPASEPVKILDTPEKLDLFTTELQKTIYVIEGTSKODLTSPNMELSSSGISADLSR 360
Qy      361  GHAVVAGAVGAKDMAGFLDLKADLQDDTFIGNEBLTPBEVAGYLGIVTWMPSROKTSLL 420
Db      361  GHAVVAGAVGAKDMAGFLDLKADLQDDTFIGNEBLTPBEVAGYLGIVTWMPSROKTSLL 420
Qy      421  ASGAPRYQHMGRVILLFQEPQGGHWSQVQTIHGQISYFGGELCGVDVDQGETELLII 480
Db      421  ASGAPRYQHMGRVILLFQEPQGGHWSQVQTIHGQISYFGGELCGVDVDQGETELLII 480
Qy      481  GAPLFYGEORGRVITYORROLGFEVSELOQDPGYPLGRFGEALTALTDINGGLADVA 540
Db      481  GAPLFYGEORGRVITYORROLGFEVSELOQDPGYPLGRFGEALTALTDINGGLADVA 540
Qy      541  VGAPLEBOGAVYIFNGRHGGLSPQSPQRIEGTQVLSGIQWFGRSIHGVKLEBGDLADVA 600

```

```

Db      541 VGAPLEBEGAVYIFNGRHGGLSPQSPQRIEGTVLSGIQWFRGRSHGVKDEGLADVA 600
Qy      601 VGASQMTVLSSRPVDMVTLMSPSPAEIPVHEVECSYSTSNKKEGVNITICFOIKSLY 660
Db      601 VGASQMTVLSSRPVDMVTLMSPSPAEIPVHEVECSYSTSNKKEGVNITICFOIKSLI 660
Qy      661 POFQGRLVANLTYTLQDGHRTTRRGLPFGGRHRLRNIAVTSMSCITDSFHFVVCYQD 720
Db      661 POFQGRLVANLTYTLQDGHRTTRRGLPFGGRHRLRNIAVTSMSCITDSFHFVVCYQD 720
Qy      721 LISPINVSINFSLWEEBGTPRDQAOQKDIPIILRPSLSHSTWEIPEFKNGCEBKCEAN 780
Db      721 LISPINVSINFSLWEEBGTPRDQAOQKDIPIILRPSLSHSTWEIPEFKNGCEBKCEAN 780
Qy      781 LRVSPSPARSRLRLTAFAASLSVELSLNLEEDAYWQDLHFPGLSFRKVEMLKPHSQ 840
Db      781 LRVSPSPARSRLRLTAFAASLSVELSLNLEEDAYWQDLHFPGLSFRKVEMLKPHSQ 840
Qy      841 IPVSCBELPESRRLSRALSCNVSSPIFKAGHSVALQMMFTLVNNSWGDVIELHANVTC 900
Db      841 IPVSCBELPESRRLSRALSCNVSSPIFKAGHSVALQMMFTLVNNSWGDVIELHANVTC 900
Qy      901 NNEDSDLEDNSATTIIPILYPINILIQDOEDSTLYVSTFKPKGIHQVKMYO----- 954
Db      901 NNEDSDLEDNSATTIIPILYPINILIQDOEDSTLYVSTFKPKGIHQVKMYO----- 954
Qy      955 -----VRIPSIDHNIP 967
Db      955 -----VRIPSIDHNIP 967
Qy      961 EMQSKQILCRPAGDAEHTVGAQGEELPCPMGVSEAPFNDIRAGCRIRIQPSIDHNIP 1020
Db      961 EMQSKQILCRPAGDAEHTVGAQGEELPCPMGVSEAPFNDIRAGCRIRIQPSIDHNIP 1020
Qy      968 TLBAVGVIPQPSBEPITHQSVQMEPPVCHYEDELRLPDAEPCLPQALFRCPVFRQ 1027
Db      968 TLBAVGVIPQPSBEPITHQSVQMEPPVCHYEDELRLPDAEPCLPQALFRCPVFRQ 1027
Qy      1021 TLBAVGVIPQPSBEPITHQSVQMEPPVCHYEDELRLPDAEPCLPQALFRCPVFRQ 1080
Db      1021 TLBAVGVIPQPSBEPITHQSVQMEPPVCHYEDELRLPDAEPCLPQALFRCPVFRQ 1080
Qy      1028 EILVQVISTLELYGIEASMSPLCSSISFNSSKHHLVGSNLSLAQVMKDVVYEX 1087
Db      1028 EILVQVISTLELYGIEASMSPLCSSISFNSSKHHLVGSNLSLAQVMKDVVYEX 1087
Qy      1081 EILVQVISTLELYGIEASMSPLCSSISFNSSKHHLVGSNLSLAQVMKDVVYEX 1140
Db      1081 EILVQVISTLELYGIEASMSPLCSSISFNSSKHHLVGSNLSLAQVMKDVVYEX 1140
Qy      1088 QMLVLYVLSIGIGLLLLIPIVLYKVGFPKNLKEMKAGRGVNGIPIAEDSEQLASQ 1147
Db      1088 QMLVLYVLSIGIGLLLLIPIVLYKVGFPKNLKEMKAGRGVNGIPIAEDSEQLASQ 1147
Qy      1141 QMLVLYVLSIGIGLLLLIPIVLYKVGFPKNLKEMKAGRGVNGIPIAEDSEQLASQ 1200
Db      1141 QMLVLYVLSIGIGLLLLIPIVLYKVGFPKNLKEMKAGRGVNGIPIAEDSEQLASQ 1200
Qy      1148 EADPGCLPLHEKDSGSGKMD 1170
Db      1148 EADPGCLPLHEKDSGSGKMD 1170
Qy      1201 EADPGCLPLHEKDSGSGKMD 1223
Db      1201 EADPGCLPLHEKDSGSGKMD 1223

```

## RESULT 11

```

US-10-473-127-1736
; Sequence 1736, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zyds Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1736

```

```

; LENGTH: 1223
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1736
Query Match      99.1%; Score 6053.5; DB 16; Length 1223;
Best Local Similarity 95.5%; Pred. No. 0;
Matches 1168; Conservative 0; Mismatches 2; Indels 53; Gaps 1;
Qy      1 MKDSCITVMAMALLSGFFPAPASSYNLDVGARSFSPPRAGRHFGYRVIOVNGVTVGA 60
Db      1 MKDSCITVMAMALLSGFFPAPASSYNLDVGARSFSPPRAGRHFGYRVIOVNGVTVGA 60
Qy      61 PGENSGTSLYQCCSGTGCHCPTLRLSNTSKTLGHTLATDPDGSILACDPGLSRCD 120
Db      61 PGENSGTSLYQCCSGTGCHCPTLRLSNTSKTLGHTLATDPDGSILACDPGLSRCD 120
Qy      121 QNTYLSGLCYLFRONLQPMLOGRPGFOECIKGNVDLVLEPDGSMISLOPDEFOKILDPMK 180
Db      121 QNTYLSGLCYLFRONLQPMLOGRPGFOECIKGNVDLVLEPDGSMISLOPDEFOKILDPMK 180
Qy      181 DVMKLSTNTSYQFAAVQFSTSYKTEPDSYVKKRBDALIKHYKMLLTNTEGAINVY 240
Db      181 DVMKLSTNTSYQFAAVQFSTSYKTEPDSYVKKRBDALIKHYKMLLTNTEGAINVY 240
Qy      241 ATEVFRBELGARPATVYLIIITDGEATDSCNIDAADIIRYIIIGIKHFQTKESOSTLH 300
Db      241 ATEVFRBELGARPATVYLIIITDGEATDSCNIDAADIIRYIIIGIKHFQTKESOSTLH 300
Qy      301 KEASKPASEPFIKIDTEKDKDLFTELQKKIYVEGTSKODLSFNNELSSGISAIDSR 360
Db      301 KEASKPASEPFIKIDTEKDKDLFTELQKKIYVEGTSKODLSFNNELSSGISAIDSR 360
Qy      361 GHAVAVGAGADWAGCELDLAKADIDPTFIGNEBLTEVEBAGVLYGTVTMLPSRQKTSLL 420
Db      361 GHAVAVGAGADWAGCELDLAKADIDPTFIGNEBLTEVEBAGVLYGTVTMLPSRQKTSLL 420
Qy      421 ASGAPRYOHNGRVLLFQEPQGGHWSOVQTIHGTQISYFGEELCGVDVDDGETELLII 480
Db      421 ASGAPRYOHNGRVLLFQEPQGGHWSOVQTIHGTQISYFGEELCGVDVDDGETELLII 480
Qy      481 GAPIFYBQGGRGVFIYORROLGFEVSELOGDGYLGRGEXALTLDINSGGLDVVA 540
Db      481 GAPIFYBQGGRGVFIYORROLGFEVSELOGDGYLGRGEXALTLDINSGGLDVVA 540
Qy      541 VGAPLEBQAVYIFNGRHGGLSPQSPQRIEGTVLSGIQWFRGRSHGVKDEGLADVA 600
Db      541 VGAPLEBQAVYIFNGRHGGLSPQSPQRIEGTVLSGIQWFRGRSHGVKDEGLADVA 600
Qy      601 VGASQMTVLSSRPVDMVTLMSPSPAEIPVHEVECSYSTSNKKEGVNITICFOIKSLY 660
Db      601 VGASQMTVLSSRPVDMVTLMSPSPAEIPVHEVECSYSTSNKKEGVNITICFOIKSLI 660
Qy      661 POFQGRLVANLTYTLQDGHRTTRRGLPFGGRHRLRNIAVTSMSCITDSFHFVVCYQD 720
Db      661 POFQGRLVANLTYTLQDGHRTTRRGLPFGGRHRLRNIAVTSMSCITDSFHFVVCYQD 720
Qy      721 LISPINVSINFSLWEEBGTPRDQAOQKDIPIILRPSLSHSTWEIPEFKNGCEBKCEAN 780
Db      721 LISPINVSINFSLWEEBGTPRDQAOQKDIPIILRPSLSHSTWEIPEFKNGCEBKCEAN 780
Qy      781 LRVSPSPARSRLRLTAFAASLSVELSLNLEEDAYWQDLHFPGLSFRKVEMLKPHSQ 840
Db      781 LRVSPSPARSRLRLTAFAASLSVELSLNLEEDAYWQDLHFPGLSFRKVEMLKPHSQ 840
Qy      841 IPVSCBELPESRRLSRALSCNVSSPIFKAGHSVALQMMFTLVNNSWGDVIELHANVTC 900
Db      841 IPVSCBELPESRRLSRALSCNVSSPIFKAGHSVALQMMFTLVNNSWGDVIELHANVTC 900
Qy      901 NNEDSDLEDNSATTIIPILYPINILIQDOEDSTLYVSTFKPKGIHQVKMYO----- 954
Db      901 NNEDSDLEDNSATTIIPILYPINILIQDOEDSTLYVSTFKPKGIHQVKMYO----- 954

```

Qy 955 -----VRIOPSIHDP 967  
Db 961 EMOTSKQLLCRPAAGAEHTVGAOGBELPCPMGVSEAPRDNIRAGPCRVRIQPSIHDP 1020  
Qy 968 TLEAVVGPQPPSEBPITHOMSVQMBEPVPCHEDELELPDAECLFGALFRCPVVRQ 1027  
Db 1021 TLEAVVGPQPPSEBPITHOMSVQMBEPVPCHEDELELPDAECLFGALFRCPVVRQ 1080  
Qy 1028 ELIVOVITLLEVEIEASMSFSLCSSISIFNSKHFHLYGSNLSLAQVVMKDVVYK 1087  
Db 1081 ELIVOVITLLEVEIEASMSFSLCSSISIFNSKHFHLYGSNLSLAQVVMKDVVYK 1140  
Qy 1088 QMLYLYVLSIGILLLLIFIVLYKVGFPKRNLEKKNAGRGVNGI PAEDSEGLASGQ 1147  
Db 1141 QMLYLYVLSIGILLLLIFIVLYKVGFPKRNLEKKNAGRGVNGI PAEDSEGLASGQ 1200  
Qy 1148 EAGDPGCLKPLHEKXDESGGKD 1170  
Db 1201 EAGDPGCLKPLHEKXDESGGKD 1223

## RESULT 12

US-10-872-198-130  
; Sequence 130, Application US/10872198  
; Publication No. US20050002897A1  
; GENERAL INFORMATION:  
; APPLICANT: Ulrich HAUPTS  
; APPLICANT: Andre KOLTERMANN  
; APPLICANT: Christiaan VOETSMER  
; APPLICANT: Ulrich Ketting  
; TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF  
; FILE REFERENCE: 04156.0002U4  
; CURRENT APPLICATION NUMBER: US/10/872,198  
; CURRENT FILING DATE: 2004-06-18  
; PRIOR FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: 60/543,518  
; PRIOR FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: 60/524,960  
; PRIOR FILING DATE: 2003-11-25  
; PRIOR APPLICATION NUMBER: EP 04003058  
; PRIOR FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: EP 03025871  
; PRIOR FILING DATE: 2003-11-11  
; PRIOR APPLICATION NUMBER: EP 03025851  
; PRIOR FILING DATE: 2003-11-10  
; PRIOR APPLICATION NUMBER: EP 03013819  
; PRIOR FILING DATE: 2003-06-18  
; NUMBER OF SEQ ID NOS: 149  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 130  
; LENGTH: 1145  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-872-198-130

Query Match 98.0%; Score 5981; DB 17; Length 1145;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 YNLDVRGARSPSPRAGHFGYRVLOVANGVIVGAPGSGNSTGSIYQCSGTGHCPLVTL 85  
Db 1 YNLDVRGARSPSPRAGHFGYRVLOVANGVIVGAPGSGNSTGSIYQCSGTGHCPLVTL 60  
Qy 86 RGSNTSTKYLMTATLTDPTDSSILACDPGLSRTCDQNTYLSGLCYLFRONTLQGPMLQGRP 145  
Db 61 RGSNTSTKYLMTATLTDPTDSSILACDPGLSRTCDQNTYLSGLCYLFRONTLQGPMLQGRP 120  
Qy 146 GFOECIKGNVDLVFLFDGSMSLQDPEFOKILDFMKDVWKKLSNTSYQPAAVOFSTSYKTE 205  
Db 121 GFOECIKGNVDLVFLFDGSMSLQDPEFOKILDFMKDVWKKLSNTSYQPAAVOFSTSYKTE 180  
Qy 206 FDFSDYVRKQPDALLKHKVKKMLLTNTFGAINVYATEVFEELGARDATKVLIIITDG 265  
Db 206 FDFSDYVRKQPDALLKHKVKKMLLTNTFGAINVYATEVFEELGARDATKVLIIITDG 265

Db 181 FDFSDYVRKQPDALLKHKVKKMLLTNTFGAINVYATEVFEELGARDATKVLIIITDG 240  
Qy 266 EATSGNIDAKODIRYIIGIKGHFOTKESQETLHKRASDPASFPVLIITPEKLDLFT 325  
Db 241 EATSGNIDAKODIRYIIGIKGHFOTKESQETLHKRASDPASFPVLIITPEKLDLFT 300  
Qy 326 ELQKKIVIBGTSKODLTSFNMELSSSGISADLSRGAHVAVGAKOMAGFLDLKADLQ 385  
Db 301 ELQKKIVIBGTSKODLTSFNMELSSSGISADLSRGAHVAVGAKOMAGFLDLKADLQ 360  
Qy 386 DDTFTIGNEPLTPEVRAQYLYTWTWPLSRQKTSILASGARRYOMGVLLFOEPQGGGW 445  
Db 361 DDTFTIGNEPLTPEVRAQYLYTWTWPLSRQKTSILASGARRYOMGVLLFOEPQGGGW 420  
Qy 446 SOVOTHTGTOIGSFGEELGVDVDQGETELLIGAPLYPYGEOGRGVFTYORRQGF 505  
Db 421 SOVOTHTGTOIGSFGEELGVDVDQGETELLIGAPLYPYGEOGRGVFTYORRQGF 480  
Qy 506 EVSELQDPCYPLGRFGEAITTALTDINGDLVDVAVGAPLEBQAVYIFNGRHGSLPOP 565  
Db 481 EVSELQDPCYPLGRFGEAITTALTDINGDLVDVAVGAPLEBQAVYIFNGRHGSLPOP 540  
Qy 566 SQRLEGTOVLSGIOWPGRSIRHGVKDLBGDGLADVAVGASQMTVLSRPVVDWTLMSFS 625  
Db 541 SQRLEGTOVLSGIOWPGRSIRHGVKDLBGDGLADVAVGASQMTVLSRPVVDWTLMSFS 600  
Qy 626 PAIIPVHEVCSTYSNKKMGVNTICFOIKSLYPOFOGRVANLTYTQLDGRTRRR 685  
Db 601 PAIIPVHEVCSTYSNKKMGVNTICFOIKSLYPOFOGRVANLTYTQLDGRTRRR 660  
Qy 686 GLFPGGHELRNIAVTTSMSCDTSFHPFVQVDLISPINVSINFSLMBEETPRDQRA 745  
Db 661 GLFPGGHELRNIAVTTSMSCDTSFHPFVQVDLISPINVSINFSLMBEETPRDQRA 720  
Qy 746 QGKDIPTILRPSLSHSEWETIPPEKNCGBDKCCANLAVSSPARRALRTAFASLSVEL 805  
Db 721 QGKDIPTILRPSLSHSEWETIPPEKNCGBDKCCANLAVSSPARRALRTAFASLSVEL 780  
Qy 806 SLSTNLEBDAYWQDLHFPPLGSLFRKYEMLKPHSQIPVSCBELPEBSRLSRLASCNVSS 865  
Db 781 SLSTNLEBDAYWQDLHFPPLGSLFRKYEMLKPHSQIPVSCBELPEBSRLSRLASCNVSS 840  
Qy 866 PIFRAGHVALQWMTLVNNSWGDSEVLEHANTYCNNEBDDLLEDSATTTIPLYPINI 925  
Db 841 PIFRAGHVALQWMTLVNNSWGDSEVLEHANTYCNNEBDDLLEDSATTTIPLYPINI 900  
Qy 926 LIQDQEDSTLYVSETPKGPXKHQYKAMYQVRIQPSIHDPNIPITLEAVVGPQPPSEBPIT 985  
Db 901 LIQDQEDSTLYVSETPKGPXKHQYKAMYQVRIQPSIHDPNIPITLEAVVGPQPPSEBPIT 960  
Qy 986 HONSVQMBEPVPCHEDELELPDAEBCPLPGALFRCPVVRROELIVOVITLLEVEIEA 1045  
Db 961 HONSVQMBEPVPCHEDELELPDAEBCPLPGALFRCPVVRROELIVOVITLLEVEIEA 1020  
Qy 1046 SSMFSLCSSISIFNSKHFHLYGSNLSLAQVVMKDVVYKQMLYLYVLSIGILLLL 1105  
Db 1021 SSMFSLCSSISIFNSKHFHLYGSNLSLAQVVMKDVVYKQMLYLYVLSIGILLLL 1080  
Qy 1106 LIPIVLYKVGFPKRNLEKKNAGRGVNGI PAEDSEGLASGOBAGDPGCLKPLHEKXSES 1165  
Db 1081 LIPIVLYKVGFPKRNLEKKNAGRGVNGI PAEDSEGLASGOBAGDPGCLKPLHEKXSES 1140  
Qy 1166 GGGKD 1170  
Db 1141 GGGKD 1145

## RESULT 13

US-11-021-951-130  
; Sequence 130, Application US/11021951  
; Publication No. US20050175581A1  
; GENERAL INFORMATION:  
; APPLICANT: HAUPTS, Ulrich

APPLICANT: KOLTERMANN, Andre  
APPLICANT: SCHEIDIG, Andreas  
APPLICANT: VOTSMEIER, Christian  
APPLICANT: Ketting, Ulrich  
APPLICANT: COCO, Wayne Michael  
TITLE OF INVENTION: New Biological Entities And The Pharmaceutical  
FILE REFERENCE: 04156.0002U5  
CURRENT APPLICATION NUMBER: US/11/021,951  
CURRENT FILING DATE: 2004-12-22  
PRIOR APPLICATION NUMBER: 10/872,198  
PRIOR FILING DATE: 2004-06-18  
PRIOR APPLICATION NUMBER: 60/543,518  
PRIOR FILING DATE: 2004-02-11  
PRIOR APPLICATION NUMBER: 60/524,960  
PRIOR FILING DATE: 2003-11-25  
PRIOR APPLICATION NUMBER: EP 04003058  
PRIOR FILING DATE: 2004-02-11  
PRIOR APPLICATION NUMBER: EP 03025871  
PRIOR FILING DATE: 2003-11-11  
PRIOR APPLICATION NUMBER: EP 03025851  
PRIOR FILING DATE: 2003-11-10  
PRIOR APPLICATION NUMBER: EP 03013819  
PRIOR FILING DATE: 2003-06-18  
NUMBER OF SEQ ID NOS: 191  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 130  
LENGTH: 1145.  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-021-951-130

Query Match 98.0%; Score 5981; DB 20; Length 1145;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 YNLDVRGARSSEPPRAAGFRGVRVQVNGVYVGAAPGEGNSGSLYQCGSGTGHCLPPTL 85  
DB 1 YNLDVRGARSFSPRAGRFGRVLYQVNGVYVGAAPGEGNSGSLYQCGSGTGHCLPPTL 60  
QY 86 RGSNTSKYLGWTLATDPTDGSLLACDPGLSRTCDONTLSGLCYLFRONTLQGPMLQGRP 145  
DB 61 RGSNTSKYLGWTLATDPTDGSLLACDPGLSRTCDONTLSGLCYLFRONTLQGPMLQGRP 120  
QY 146 GFQECIKGNVDVLPFDGSMSLQDPDFOKILDFMKDVVKKLSNTSYQFAAVQFSTSYKTE 205  
DB 121 GFQECIKGNVDVLPFDGSMSLQDPDFOKILDFMKDVVKKLSNTSYQFAAVQFSTSYKTE 180  
QY 206 PFDSDYVRKDDPDLALIKVKNMLLTNTFGAINVYATEVFEELGARPATVLLIITDG 265  
DB 181 PFDSDYVRKDDPDLALIKVKNMLLTNTFGAINVYATEVFEELGARPATVLLIITDG 240  
QY 266 EATDGNIDAAKOIIRYIIGIKGHFOTKESQETLHKFKSKPSEVFKILDTREKLDKDTFT 325  
DB 241 EATDGNIDAAKOIIRYIIGIKGHFOTKESQETLHKFKSKPSEVFKILDTREKLDKDTFT 300  
QY 326 ELQKKIYVIEGTSKODLTSFNMELSSSGISADLSRGAHVGAAGKADWAGFLDKADQ 385  
DB 301 ELQKKIYVIEGTSKODLTSFNMELSSSGISADLSRGAHVGAAGKADWAGFLDKADQ 360  
QY 366 DDTFGNEPLTEVRAGVGYTVTWLPSRQKTSLLASGAPRYOHMGVLLFQEPQGGHW 445  
DB 361 DDTFGNEPLTEVRAGVGYTVTWLPSRQKTSLLASGAPRYOHMGVLLFQEPQGGHW 420  
QY 446 SOVOTIHGRIQISYFGEGLGVDVODDGETELLIGAPLFYGEORHGRVITYOROLGHE 505  
DB 421 SOVOTIHGRIQISYFGEGLGVDVODDGETELLIGAPLFYGEORHGRVITYOROLGHE 480  
QY 506 EYSELQGDGPGYPLRGGAITALTIDINGDLVVAVGAPLEBOGAVYIFNGRHGGLSPDP 565  
DB 481 EYSELQGDGPGYPLRGGAITALTIDINGDLVVAVGAPLEBOGAVYIFNGRHGGLSPDP 540  
QY 566 SORIEGTQVLSGIQMFGRSHGVKDLBGDLADVAVGAESQMTVLSRPVVDMTLMSFS 625

DB 541 SORIEGTQVLSGIQMFGRSHGVKDLBGDLADVAVGAESQMTVLSRPVVDMTLMSFS 600  
QY 626 PAEIPVHEVECSYSTSNKMEGVNITTCFOIKSLYPOFQGLVANLTYTLOLDGRTTTR 685  
DB 601 PAEIPVHEVECSYSTSNKMEGVNITTCFOIKSLYPOFQGLVANLTYTLOLDGRTTTR 660  
QY 686 GLPFGGRHELRNNAVTTSNCTDPSFHPVQVODLSPINVSINFSIMEEGTPROORA 745  
DB 661 GLPFGGRHELRNNAVTTSNCTDPSFHPVQVODLSPINVSINFSIMEEGTPROORA 720  
QY 746 QGKDIPILRSLHSETEWIEPFERNKCGEDKCEANLRVSFSPASRALRTAFASLSEVL 805  
DB 721 QGKDIPILRSLHSETEWIEPFERNKCGEDKCEANLRVSFSPASRALRTAFASLSEVL 780  
QY 806 SLNLSEEDAYVQDLHPPLGSLSPKXVEMLRPHSQIIPVSCLELPEESRLSRALSCNVSS 865  
DB 781 SLNLSEEDAYVQDLHPPLGSLSPKXVEMLRPHSQIIPVSCLELPEESRLSRALSCNVSS 840  
QY 866 PIFRAGSHVALQMMFNTLVNSKGDVSLHANVTCNNEDSDLLDENSATYTIIPILYPTNI 925  
DB 841 PIFRAGSHVALQMMFNTLVNSKGDVSLHANVTCNNEDSDLLDENSATYTIIPILYPTNI 900  
QY 926 LIQDQEDSTLYVSFTPKGPKIHQVKNVQVRIOPSIHQHNIPTEBAVVGVPQPSGPT 985  
DB 901 LIQDQEDSTLYVSFTPKGPKIHQVKNVQVRIOPSIHQHNIPTEBAVVGVPQPSGPT 960  
QY 986 HOMSVOEMPVPCHYEDELRLPDAAEPCLPGALFRCPVFRQEIIVQYIGTLBELVGEIEA 1045  
DB 961 HOMSVOEMPVPCHYEDELRLPDAAEPCLPGALFRCPVFRQEIIVQYIGTLBELVGEIEA 1020  
QY 1046 SSMFSLCSSLISIFSNSSKHFLYGSNMSLAQVNVKVDVYKQMLYVLSIGGLILL 1105  
DB 1021 SSMFSLCSSLISIFSNSSKHFLYGSNMSLAQVNVKVDVYKQMLYVLSIGGLILL 1080  
QY 1106 LIFTLYKVGFPKXNLKEMKAGRGVPGIQAEDSEQLASQEZGDPGCLPLHKOSES 1165  
DB 1081 LIFTLYKVGFPKXNLKEMKAGRGVPGIQAEDSEQLASQEZGDPGCLPLHKOSES 1140  
QY 1166 GGGKD 1170  
DB 1141 GGGKD 1145  
RESULT 14  
US-10-473-127-1738  
Sequence 1738, Application US/10473127  
Publication No. US20040236091A1  
GENERAL INFORMATION:  
APPLICANT: Zycos Inc.  
TITLE OF INVENTION: TRANSLATIONAL PROFILING  
FILE REFERENCE: 08191-026W01  
CURRENT APPLICATION NUMBER: US/10/473,127  
CURRENT FILING DATE: 2003-09-26  
PRIOR APPLICATION NUMBER: 60/279,495  
PRIOR FILING DATE: 2001-03-28  
PRIOR APPLICATION NUMBER: 60/292,544  
PRIOR FILING DATE: 2001-05-21  
PRIOR APPLICATION NUMBER: 60/310,801  
PRIOR FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: 60/326,370  
PRIOR FILING DATE: 2001-10-01  
PRIOR APPLICATION NUMBER: 60/336,780  
PRIOR FILING DATE: 2001-12-04  
PRIOR APPLICATION NUMBER: 60/358,985  
PRIOR FILING DATE: 2002-02-20  
NUMBER OF SEQ ID NOS: 2041  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1738  
LENGTH: 1145  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-473-127-1738

Query Match 97.8%; Score 5973; DB 16; Length 1145;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1144; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 26 YNLVDRGARSPSPRAGHFGYRVLOVNGVYVGAPEGNGTSGSYQCGSTGHCPLPTL 85  
 DB 1 YNLDRGARSPSPRAGHFGYRVLOVNGVYVGAPEGNGTSGSYQCGSTGHCPLPTL 60  
 QY 86 RGSNTSYKLGWTLATDPTDGSIIACDPGLSRTCPQNTYLSGLCYLFPQNTQGPMLQGRP 145  
 DB 61 RGSNTSYKLGWTLATDPTDGSIIACDPGLSRTCPQNTYLSGLCYLFPQNTQGPMLQGRP 120  
 QY 146 GFOECIKGNVDLVFLFDGSMSLQDPDEFQKILDFMDVWKKLSNTSYQFAAVQFSTYKTE 205  
 DB 121 GFOECIKGNVDLVFLFDGSMSLQDPDEFQKILDFMDVWKKLSNTSYQFAAVQFSTYKTE 180  
 QY 206 PDPSTYVYKRPDALLKIVKMLLTNTFGAINVYATVFEELGAPDARKVLIIITDG 265  
 DB 181 PDPSTYVYKRPDALLKIVKMLLTNTFGAINVYATVFEELGAPDARKVLIIITDG 240  
 QY 266 EATSGNIDAAKDIIRYIIGIKHQTKESQETLHKFASKPASEPVKILDTPEKLDKDLFT 325  
 DB 241 EATSGNIDAAKDIIRYIIGIKHQTKESQETLHKFASKPASEPVKILDTPEKLDKDLFT 300  
 QY 326 ELQKKIYIEGTSKQDLTSFNMELSSSGISADLSRGHVVGAQKADWAGGFLDLKADLQ 385  
 DB 301 ELQKKIYIEGTSKQDLTSFNMELSSSGISADLSRGHVVGAQKADWAGGFLDLKADLQ 360  
 QY 386 DDTFIGNEPILPEVRAGLYGTTVTWLBRSQRTSLASGAPRYOHMGVLLFOEPQGGGHW 445  
 DB 361 DDTFIGNEPILPEVRAGLYGTTVTWLBRSQRTSLASGAPRYOHMGVLLFOEPQGGGHW 420  
 QY 446 SOVQIHGTQIGSYGGELCGVDVQDGETELLIGALFLYGEORGGVLFYORROGFE 505  
 DB 421 SOVQIHGTQIGSYGGELCGVDVQDGETELLIGALFLYGEORGGVLFYORROGFE 480  
 QY 506 EVSBLQDGPYPLGFGFEGALITLTDINGDLVDVAVGAPLEBOGAVYIFNGRHGGLSPQ 565  
 DB 481 EVSBLQDGPYPLGFGFEGALITLTDINGDLVDVAVGAPLEBOGAVYIFNGRHGGLSPQ 540  
 QY 566 SQRLEGTOVLSGIGQFGRSIHGVKDLBDGLADVAVGAESQMTIVLSSRPVDMWTMSFS 625  
 DB 541 SQRLEGTOVLSGIGQFGRSIHGVKDLBDGLADVAVGAESQMTIVLSSRPVDMWTMSFS 600  
 QY 626 PABIVHEVGSYSNMGKEGVNTTCFOIKSLYPOQGRVAVLTATTLTLDGHRTRR 685  
 DB 601 PABIVHEVGSYSNMGKEGVNTTCFOIKSLYPOQGRVAVLTATTLTLDGHRTRR 660  
 QY 686 GLFGRHELRNIAVTTSMSCDTPSFHFPVCVODLISPIVNSLNFSLMBEGTPRDORA 745  
 DB 661 GLFGRHELRNIAVTTSMSCDTPSFHFPVCVODLISPIVNSLNFSLMBEGTPRDORA 720  
 QY 746 QGKQIPILRPLSLHSETWELPEKXNGGDKCEANLRVFSGPARSARALRTAFASLVEL 805  
 DB 721 QGKQIPILRPLSLHSETWELPEKXNGGDKCEANLRVFSGPARSARALRTAFASLVEL 780  
 QY 806 SLSTLBERAAVVOJDLHFRPGLSRKXVEMLKPHSGQIPVSCRELPEBSLLSRALSQVSS 865  
 DB 781 SLSTLBERAAVVOJDLHFRPGLSRKXVEMLKPHSGQIPVSCRELPEBSLLSRALSQVSS 840  
 QY 866 PIFKAGSHVALQMMFNTLVNSWGDVVELHANVTCNNDSPLLEBNSATIIIPILYPINI 925  
 DB 841 PIFKAGSHVALQMMFNTLVNSWGDVVELHANVTCNNDSPLLEBNSATIIIPILYPINI 900  
 QY 926 LIQDQDSTLYVSTPKGPKIHQVKNYQVRIQPSIHDANIPTLEAVVGVQPSSEGIT 985  
 DB 901 LIQDQDSTLYVSTPKGPKIHQVKNYQVRIQPSIHDANIPTLEAVVGVQPSSEGIT 960  
 QY 986 HGWVQNEPVPVCHYEDLERLPDAABPCLRGALFRCPVFRQBIIVQYITGLLELVGEIEA 1045  
 DB 961 HGWVQNEPVPVCHYEDLERLPDAABPCLRGALFRCPVFRQBIIVQYITGLLELVGEIEA 1020

QY 1046 SSMFSLCSLSISENSSKHFHLVGSNASLAAQVWVKVDVVEKQMLYLYVLSGIGLLLL 1105  
 DB 1021 SSMFSLCSLSISENSSKHFHLVGSNASLAAQVWVKVDVVEKQMLYLYVLSGIGLLLL 1080  
 QY 1106 LIFIVLYKVGFPKRNLEKKNBAGRGVNPNGIIPADSEQLASGQADPGCLKPLHEKSES 1165  
 DB 1081 LIFIVLYKVGFPKRNLEKKNBAGRGVNPNGIIPADSEQLASGQADPGCLKPLHEKSES 1140  
 QY 1166 GGGKD 1170  
 DB 1141 GGGKD 1145

RESULT 15  
 US-10-473-127-1741  
 ; Sequence 1741, Application US/10473127  
 ; Publication No. US20040236091A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Zycos Inc.  
 ; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
 ; FILE REFERENCE: 08191-026W01  
 ; CURRENT APPLICATION NUMBER: US/10/473,127  
 ; PRIOR FILING DATE: 2003-09-26  
 ; PRIOR APPLICATION NUMBER: 60/279,495  
 ; PRIOR FILING DATE: 2001-03-28  
 ; PRIOR APPLICATION NUMBER: 60/292,544  
 ; PRIOR FILING DATE: 2001-05-21  
 ; PRIOR APPLICATION NUMBER: 60/310,801  
 ; PRIOR FILING DATE: 2001-08-08  
 ; PRIOR APPLICATION NUMBER: 60/326,370  
 ; PRIOR FILING DATE: 2001-10-01  
 ; PRIOR APPLICATION NUMBER: 60/336,780  
 ; PRIOR FILING DATE: 2001-12-04  
 ; PRIOR APPLICATION NUMBER: 60/358,985  
 ; PRIOR FILING DATE: 2002-02-20  
 ; NUMBER OF SEQ ID NOS: 2041  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1741  
 ; LENGTH: 1086  
 ; TYPE: PRF  
 ; ORGANISM: Homo sapiens  
 ; US-10-473-127-1741

Query Match 92.5%; Score 5649.5; DB 16; Length 1086;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 1084; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 MKDSCITVMAMALLSGFFFPAPASVYLDVVGARSFSPRAGHFGYRVLOVNGVYVGA 60  
 DB 1 MKDSCITVMAMALLSGFFFPAPASVYLDVVGARSFSPRAGHFGYRVLOVNGVYVGA 60  
 QY 61 PGBGNSGSLYQCGSTGHCPLPTLGRSNTSKYLGTATLTDPTDGSIIACDPGLSRTCD 120  
 DB 61 PGBGNSGSLYQCGSTGHCPLPTLGRSNTSKYLGTATLTDPTDGSIIACDPGLSRTCD 120  
 QY 121 QNTYLSGLCYLFPQNTQGPMLQGRPQFQECIKGNVDLVFLFDGSMSLQDPDEFQKILDFPMK 180  
 DB 121 QNTYLSGLCYLFPQNTQGPMLQGRPQFQECIKGNVDLVFLFDGSMSLQDPDEFQKILDFPMK 180  
 QY 181 DVWKKLSNTSYQFAAVQFSTYKTEPDPFSDYVRKDPDALLKIVKMLLTNTFGAINVY 240  
 DB 181 DVWKKLSNTSYQFAAVQFSTYKTEPDPFSDYVRKDPDALLKIVKMLLTNTFGAINVY 240  
 QY 241 ATEVFEELGAPDARKVLIIITDGEATDSGNIDAAKDIIRYIIGIKHQTKESQETLH 300  
 DB 241 ATEVFEELGAPDARKVLIIITDGEATDSGNIDAAKDIIRYIIGIKHQTKESQETLH 300  
 QY 301 KPASKPASEPVKILDTPEKLDKDLFTLEOKKIYVIBGTSKQDLTSFNMELSSSGISADLSR 360  
 DB 301 KPASKPASEPVKILDTPEKLDKDLFTLEOKKIYVIBGTSKQDLTSFNMELSSSGISADLSR 360  
 QY 361 GHAUVGAVGADWAGGFLDLKADLQDDTFIGNEPILPEVRAGLYGTTVTWLBRSQRTSL 420

Db 361 CHAVVAVGAKDMAGGFLDLKADLDDFEIGNRPLTPEVRAGYLGYTVTWLPSRQKTSLL 420  
QY 421 ASDAPRYOMGRVLLFOEPQGGGHSQVOTIHGTQISFGGELCGVDVDQGETELLII 480  
Db 421 ASGARPYOMGRVLLFOEPQGGGHSQVOTIHGTQISFGGELCGVDVDQGETELLII 480  
QY 481 GAPLFYGEORGRVFIYQRRLGFEEVSELQDPGYPLGRFGEAITALTIDINGDLADVA 540  
Db 481 GAPLFYGEORGRVFIYQRRLGFEEVSELQDPGYPLGRFGEAITALTIDINGDLADVA 540  
QY 541 VGAPLEBQAVYIFNGRHGGLSPQSORLEGTVLSGIQWFGRSIHGVKDLBGDLADVA 600  
Db 541 VGAPLEBQAVYIFNGRHGGLSPQSORLEGTVLSGIQWFGRSIHGVKDLBGDLADVA 600  
QY 601 VGAESQMTVLSRFPVDMWTLMSPSPAEIPIHEVECSYSTSNKKEGVNITTCFOIKSLY 660  
Db 601 VGAESQMTVLSRFPVDMWTLMSPSPAEIPIHEVECSYSTSNKKEGVNITTCFOIKSLI 660  
QY 661 POFQGRLVANLTYTLOLDGHTRRRGLFPGGRHELRRNIAVTTSMSCDTFSFHPVCVOD 720  
Db 661 POFQGRLVANLTYTLOLDGHTRRRGLFPGGRHELRRNIAVTTSMSCDTFSFHPVCVOD 720  
QY 721 LISPIVNSLNFSLWEEBGTFRDQAGKDIPIILRPSLHSETWEIPIFEKNCGEDKKEAN 780  
Db 721 LISPIVNSLNFSLWEEBGTFRDQAGKDIPIILRPSLHSETWEIPIFEKNCGEDKKEAN 780  
QY 781 LRVSPSPARSLRLTAFASLSVELSLNLEBDAYWQDLHFPPLGSLFRKYEMLKPHSQ 840  
Db 781 LRVSPSPARSLRLTAFASLSVELSLNLEBDAYWQDLHFPPLGSLFRKYEMLKPHSQ 840  
QY 841 IPVSGCELPEBSRLSRALSCNVSSPIPKAGHVALQMMFNTLVNNSWGDSTELHANTYC 900  
Db 841 IPVSGCELPEBSRLSRALSCNVSSPIPKAGHVALQMMFNTLVNNSWGDSTELHANTYC 900  
QY 901 NNHSDLDLEDNSATTIIPILYINILIOEDNSTLYVSFTPKGPKHQVKMYQVRIOPS 960  
Db 901 NNHSDLDLEDNSATTIIPILYINILIOEDNSTLYVSFTPKGPKHQVKMYQVRIOPS 960  
QY 961 IHDHNIPTLEAVGVPOPPSEGPITHQWSVQMEPPVPCHYEDLERLPDAEPCLPALFR 1020  
Db 961 IHDHNIPTLEAVGVPOPPSEGPITHQWSVQMEPPVPCHYEDLERLPDAEPCLPALFR 1020  
QY 1021 CPVVRORLIVQITGLVGEIEASMSPLCSSLISFNSSKHPHLYGSNLSLAQVVMK 1080  
Db 1021 CPVVRORLIVQITGLVGEIEASMSPLCSSLISFNSSKHPHLYGSNLSLAQVVMK 1080  
QY 1081 VDVVYEX 1087  
Db 1081 VDVVYEX 1086

Search completed: August 29, 2005, 19:27:27  
Job time : 184 secs



***This Page Blank (uspto)***

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 29, 2005, 19:20:14 ; Search time 483 Seconds

(without alignments)  
2829.332 Million cell updates/sec

Title: US-09-945-265-2

Perfect score: 6106  
Sequence: 1 MKDSCITTMAMALLSGFFFF.....DPGLKPLHEKDSGGGKD 1170

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA Main:\*

1: /cgn2\_6/ptodata/1/paa/PCTUS\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/paa/US06\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/paa/US07\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/paa/US08\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/paa/US081\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/paa/US082\_COMB.pep.\*  
7: /cgn2\_6/ptodata/1/paa/US083\_COMB.pep.\*  
8: /cgn2\_6/ptodata/1/paa/US084\_COMB.pep.\*  
9: /cgn2\_6/ptodata/1/paa/US085\_COMB.pep.\*  
10: /cgn2\_6/ptodata/1/paa/US086\_COMB.pep.\*  
11: /cgn2\_6/ptodata/1/paa/US087\_COMB.pep.\*  
12: /cgn2\_6/ptodata/1/paa/US088\_COMB.pep.\*  
13: /cgn2\_6/ptodata/1/paa/US089\_COMB.pep.\*  
14: /cgn2\_6/ptodata/1/paa/US090\_COMB.pep.\*  
15: /cgn2\_6/ptodata/1/paa/US091\_COMB.pep.\*  
16: /cgn2\_6/ptodata/1/paa/US092\_COMB.pep.\*  
17: /cgn2\_6/ptodata/1/paa/US093\_COMB.pep.\*  
18: /cgn2\_6/ptodata/1/paa/US094\_COMB.pep.\*  
19: /cgn2\_6/ptodata/1/paa/US095\_COMB.pep.\*  
20: /cgn2\_6/ptodata/1/paa/US096\_COMB.pep.\*  
21: /cgn2\_6/ptodata/1/paa/US097\_COMB.pep.\*  
22: /cgn2\_6/ptodata/1/paa/US097b\_COMB.pep.\*  
23: /cgn2\_6/ptodata/1/paa/US098\_COMB.pep.\*  
24: /cgn2\_6/ptodata/1/paa/US099\_COMB.pep.\*  
25: /cgn2\_6/ptodata/1/paa/US099a\_COMB.pep.\*  
26: /cgn2\_6/ptodata/1/paa/US100\_COMB.pep.\*  
27: /cgn2\_6/ptodata/1/paa/US101\_COMB.pep.\*  
28: /cgn2\_6/ptodata/1/paa/US102\_COMB.pep.\*  
29: /cgn2\_6/ptodata/1/paa/US103\_COMB.pep.\*  
30: /cgn2\_6/ptodata/1/paa/US104\_COMB.pep.\*  
31: /cgn2\_6/ptodata/1/paa/US105\_COMB.pep.\*  
32: /cgn2\_6/ptodata/1/paa/US106\_COMB.pep.\*  
33: /cgn2\_6/ptodata/1/paa/US107\_COMB.pep.\*  
34: /cgn2\_6/ptodata/1/paa/US108\_COMB.pep.\*  
35: /cgn2\_6/ptodata/1/paa/US109\_COMB.pep.\*  
36: /cgn2\_6/ptodata/1/paa/US110\_COMB.pep.\*  
37: /cgn2\_6/ptodata/1/paa/US60\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6106	100.0	1170	1 PCT-US02-09671-1743	Sequence 1743, Ap
2	6106	100.0	1170	22 US-09-791-537-83469	Sequence 83469, A
3	6106	100.0	1170	24 US-09-945-265-2	Sequence 2, Appl1
4	6106	100.0	1170	30 US-10-473-127-1743	Sequence 1743, Ap
5	6098	99.9	1170	1 PCT-US02-09671-1737	Sequence 1737, Ap
6	6098	99.9	1170	1 PCT-US02-09671-1739	Sequence 1739, Ap
7	6098	99.9	1170	1 PCT-US02-09671-1742	Sequence 1742, Ap
8	6098	99.9	1170	1 PCT-US03-12946-3007	Sequence 3007, Ap
9	6098	99.9	1170	1 PCT-US03-40978-1088	Sequence 1088, Ap
10	6098	99.9	1170	19 US-09-592-617A-42	Sequence 42, Appl
11	6098	99.9	1170	19 US-09-592-617C-42	Sequence 42, Appl
12	6098	99.9	1170	22 US-09-791-537-118794	Sequence 118794, A
13	6098	99.9	1170	27 US-10-170-205R-35754	Sequence 35754, A
14	6098	99.9	1170	28 US-10-261-164-1	Sequence 1, Appl1
15	6098	99.9	1170	29 US-10-325-899-9350	Sequence 9350, Ap
16	6098	99.9	1170	30 US-10-473-127-1737	Sequence 1737, Ap
17	6098	99.9	1170	30 US-10-473-127-1739	Sequence 1739, Ap
18	6098	99.9	1170	30 US-10-473-127-1742	Sequence 1742, Ap
19	6098	99.9	1170	33 US-10-741-600-1088	Sequence 1088, Ap
20	6098	99.9	1170	34 US-10-802-508-42	Sequence 42, Appl
21	6098	99.9	1170	36 US-11-000-473-42	Sequence 42, Appl
22	6098	99.9	1170	37 US-60-453-050-11104	Sequence 11104, A
23	6098	99.9	1170	37 US-60-453-537-11104	Sequence 118794, A
24	6098	99.9	1170	37 US-60-455-444-5811	Sequence 5811, Ap
25	6098	99.9	1170	37 US-60-465-241-5811	Sequence 5811, Ap
26	6098	99.9	1170	37 US-60-466-412-11104	Sequence 11104, A
27	6098	99.9	1170	37 US-60-474-850-513	Sequence 513, Ap
28	6098	99.9	1170	37 US-60-487-610-1880	Sequence 1880, Ap
29	6098	99.9	1170	37 US-60-548-091-382	Sequence 382, Ap
30	6098	99.9	1170	37 US-60-582-609-1880	Sequence 1880, Ap
31	6061.5	99.3	1223	1 PCT-US03-40978-1086	Sequence 1086, Ap
32	6061.5	99.3	1223	33 US-10-741-600-1086	Sequence 1086, Ap
33	6061.5	99.3	1223	7 US-60-548-091-380	Sequence 380, Ap
34	6058	99.2	1170	7 US-08-380-167-42	Sequence 42, Appl
35	6058	99.2	1170	7 US-08-380-167A-42	Sequence 42, Appl
36	6058	99.2	1170	8 US-08-476-062-42	Sequence 42, Appl
37	6053.5	99.1	1223	1 PCT-US02-09671-1736	Sequence 1736, Ap
38	6053.5	99.1	1223	22 US-09-791-537-124811	Sequence 124811, A
39	6053.5	99.1	1223	30 US-10-408-765-295	Sequence 295, Ap
40	6053.5	99.1	1223	30 US-10-408-765A-295	Sequence 295, Ap
41	6053.5	99.1	1223	30 US-10-473-127-1736	Sequence 1736, Ap
42	6053.5	99.1	1223	37 US-60-389-987-295	Sequence 295, Ap
43	6053.5	99.1	1223	37 US-60-412-418-295	Sequence 295, Ap
44	5981	98.0	1145	34 US-10-872-198-130	Sequence 130, Ap
45	5973	97.8	1145	1 PCT-US02-09671-1738	Sequence 1738, Ap

## ALIGNMENTS

RESULT 1  
PCT-US02-09671-1743  
; Sequence 1743, Application PC/TUS0209671  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: PCT/US02/09671  
; PRIOR FILING DATE: 2002-03-28  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04

;; PRIOR APPLICATION NUMBER: 60/358,985  
;; PRIOR FILING DATE: 2002-02-20  
;; NUMBER OF SEQ ID NOS: 2041  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO: 1743  
;; LENGTH: 1170  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
PCT-US02-09671-1743

Query Match 100.0%; Score 6106; DB 1; Length 1170;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MKDSCITVMAMALLSGFFFPAPASYNLDVKGARSPPRAGRHFGYRVLOVNGVTVGA 60
DB 1 MKDSCITVMAMALLSGFFFPAPASYNLDVKGARSPPRAGRHFGYRVLOVNGVTVGA 60
QY 61 PGEENSTGSLYOCOSGTGHCPLVTLRGSNTSKYLGMTLATDPTDGSILACDPGLSRTCD 120
DB 61 PGEENSTGSLYOCOSGTGHCPLVTLRGSNTSKYLGMTLATDPTDGSILACDPGLSRTCD 120
QY 121 QNTYLSGLCYLFRONTLQGPMLQGRPGQECIKGNVDLVFLFDGSMSLQDPDEFQKILDFMK 180
DB 121 QNTYLSGLCYLFRONTLQGPMLQGRPGQECIKGNVDLVFLFDGSMSLQDPDEFQKILDFMK 180
QY 181 DVMKKLSNTSYOPAAVOFSTSYKTEPDSYVKRKPDPALKKHYKMLLNTFGAIVYV 240
DB 181 DVMKKLSNTSYOPAAVOFSTSYKTEPDSYVKRKPDPALKKHYKMLLNTFGAIVYV 240
QY 241 ATEVFEELGARPDAATKVLIIITDGEATDSGNIDAANDIIRYIIGIKHPQTKESQETLH 300
DB 241 ATEVFEELGARPDAATKVLIIITDGEATDSGNIDAANDIIRYIIGIKHPQTKESQETLH 300
QY 301 KFAASKPASEPVKILDTFEKLDLFTLELOKKIYVIGTSKODLTSNMELSSSGISADLSR 360
DB 301 KFAASKPASEPVKILDTFEKLDLFTLELOKKIYVIGTSKODLTSNMELSSSGISADLSR 360
QY 361 GHAVVAVGAKDWAAGFLDLKADLQDDPTFIGNEPITPEVAGYLGTVTWLPSRQKTSLL 420
DB 361 GHAVVAVGAKDWAAGFLDLKADLQDDPTFIGNEPITPEVAGYLGTVTWLPSRQKTSLL 420
QY 421 ASGARVYOHMGRVILLFQEPQGGHMSQVOTIHGTQISYFGGELCGVVDQDGETELLII 480
DB 421 ASGARVYOHMGRVILLFQEPQGGHMSQVOTIHGTQISYFGGELCGVVDQDGETELLII 480
QY 481 GAFLEFGORGRAPVITYORROLGFEVESELQDDPGYPLGRFGEALTALTDINGDLVDVA 540
DB 481 GAFLEFGORGRAPVITYORROLGFEVESELQDDPGYPLGRFGEALTALTDINGDLVDVA 540
QY 541 VGAPLEEGGAVYIFNGRHGGLSPQPSQRIEGTQVLSGIQWFGRSIHGKDLLEGDLADVA 600
DB 541 VGAPLEEGGAVYIFNGRHGGLSPQPSQRIEGTQVLSGIQWFGRSIHGKDLLEGDLADVA 600
QY 601 VGABSQMTVLSSRPVDMVTILMSFSPAIPVHEVECSYSTSNKKKEGVNITICQIKSLY 660
DB 601 VGABSQMTVLSSRPVDMVTILMSFSPAIPVHEVECSYSTSNKKKEGVNITICQIKSLY 660
QY 661 POFQRLVANTLYTLQDLGHRTRRGLFPGGRHELRRIAVTTSCTDSFHFPPVCOD 720
DB 661 POFQRLVANTLYTLQDLGHRTRRGLFPGGRHELRRIAVTTSCTDSFHFPPVCOD 720
QY 721 LISPIVNSLNSLWEEGTPRDQRAQKDIPIILRPSLHSETWEIPEPKNGGEKKCAN 780
DB 721 LISPIVNSLNSLWEEGTPRDQRAQKDIPIILRPSLHSETWEIPEPKNGGEKKCAN 780
QY 781 LRVFSPARSALRLTAPASISVELSLNLEDAVWQDLHFPFGLSFRKYEMLKPHSQ 840
DB 781 LRVFSPARSALRLTAPASISVELSLNLEDAVWQDLHFPFGLSFRKYEMLKPHSQ 840
QY 841 IPVSCBEPERSRLISRLSCNVSSPIFKAGHSVALQMMENTLVNSSWGSDEVELHANYTC 900
DB 841 IPVSCBEPERSRLISRLSCNVSSPIFKAGHSVALQMMENTLVNSSWGSDEVELHANYTC 900
```

```
QY 901 NNEDSDLLDNSSATTIPIIYIPINILIQOQEDSTLYVSFTPKGPKIHQVGMVQVRIQPS 960
DB 901 NNEDSDLLDNSSATTIPIIYIPINILIQOQEDSTLYVSFTPKGPKIHQVGMVQVRIQPS 960
QY 961 IHDNIPITLBAVGVQPPSEEGPITTHQWSVQMEPVVPCHEDELERLDAAPCLPGALFR 1020
DB 961 IHDNIPITLBAVGVQPPSEEGPITTHQWSVQMEPVVPCHEDELERLDAAPCLPGALFR 1020
QY 1021 CPVVFROEIIIVQVGTLEIVGEIEASSMFSLCSSLISFNSSKPHLYGSNASLAQVVMK 1080
DB 1021 CPVVFROEIIIVQVGTLEIVGEIEASSMFSLCSSLISFNSSKPHLYGSNASLAQVVMK 1080
QY 1081 VDVVYERQMTLYLVLSGIGLLILLIFLYLVKVFGRMLKEKMEAGRVVNGIPAEBS 1140
DB 1081 VDVVYERQMTLYLVLSGIGLLILLIFLYLVKVFGRMLKEKMEAGRVVNGIPAEBS 1140
QY 1141 EQLASQGEADDPGCLKPLHKKDSBSGGKD 1170
DB 1141 EQLASQGEADDPGCLKPLHKKDSBSGGKD 1170

RESULT 2
US-09-791-83469
; Sequence 83469, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER
; FILE REFERENCE: 261/210
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 83469
; LENGTH: 1170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-83469

Query Match 100.0%; Score 6106; DB 22; Length 1170;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MKDSCITVMAMALLSGFFFPAPASYNLDVKGARSPPRAGRHFGYRVLOVNGVTVGA 60
DB 1 MKDSCITVMAMALLSGFFFPAPASYNLDVKGARSPPRAGRHFGYRVLOVNGVTVGA 60
QY 61 PGEENSTGSLYOCOSGTGHCPLVTLRGSNTSKYLGMTLATDPTDGSILACDPGLSRTCD 120
DB 61 PGEENSTGSLYOCOSGTGHCPLVTLRGSNTSKYLGMTLATDPTDGSILACDPGLSRTCD 120
QY 121 QNTYLSGLCYLFRONTLQGPMLQGRPGQECIKGNVDLVFLFDGSMSLQDPDEFQKILDFMK 180
DB 121 QNTYLSGLCYLFRONTLQGPMLQGRPGQECIKGNVDLVFLFDGSMSLQDPDEFQKILDFMK 180
QY 181 DVMKKLSNTSYOPAAVOFSTSYKTEPDSYVKRKPDPALKKHYKMLLNTFGAIVYV 240
DB 181 DVMKKLSNTSYOPAAVOFSTSYKTEPDSYVKRKPDPALKKHYKMLLNTFGAIVYV 240
QY 241 ATEVFEELGARPDAATKVLIIITDGEATDSGNIDAANDIIRYIIGIKHPQTKESQETLH 300
DB 241 ATEVFEELGARPDAATKVLIIITDGEATDSGNIDAANDIIRYIIGIKHPQTKESQETLH 300
QY 301 KFAASKPASEPVKILDTFEKLDLFTLELOKKIYVIGTSKODLTSNMELSSSGISADLSR 360
DB 301 KFAASKPASEPVKILDTFEKLDLFTLELOKKIYVIGTSKODLTSNMELSSSGISADLSR 360
QY 361 GHAVVAVGAKDWAAGFLDLKADLQDDPTFIGNEPITPEVAGYLGTVTWLPSRQKTSLL 420
DB 361 GHAVVAVGAKDWAAGFLDLKADLQDDPTFIGNEPITPEVAGYLGTVTWLPSRQKTSLL 420
```

QY 421 ASGAPRYOHMGRVLLFQEPQGGHMSQVOTIHGQISYFGGELCGVVDODGETELLII 480  
DB 421 ASGAPRYOHMGRVLLFQEPQGGHMSQVOTIHGQISYFGGELCGVVDODGETELLII 480  
QY 481 GAPLFYEGORGRVFIYQRRQLGFEEVSELQDPEYPLGRGFEATLTALTDINGDLVDA 540  
DB 481 GAPLFYEGORGRVFIYQRRQLGFEEVSELQDPEYPLGRGFEATLTALTDINGDLVDA 540  
QY 541 VGAPLEEQGAVYIFNGRHGGLSPQSPQRIEGTQVLSGIQWFGRSIHGVKDLBGDLADVA 600  
DB 541 VGAPLEEQGAVYIFNGRHGGLSPQSPQRIEGTQVLSGIQWFGRSIHGVKDLBGDLADVA 600  
QY 541 VGAPLEEQGAVYIFNGRHGGLSPQSPQRIEGTQVLSGIQWFGRSIHGVKDLBGDLADVA 600  
DB 541 VGAPLEEQGAVYIFNGRHGGLSPQSPQRIEGTQVLSGIQWFGRSIHGVKDLBGDLADVA 600  
QY 601 VGASQOMIVLSSRPVDMVTLMSPFPAIPVHEVECSYSTSNKKEGVNITICQIKSLY 660  
DB 601 VGASQOMIVLSSRPVDMVTLMSPFPAIPVHEVECSYSTSNKKEGVNITICQIKSLY 660  
QY 661 POFQGRIVANLTYTLQDGHRTRRGLFPGGRHRLRNIATTSMSCTDFSFPFVQVD 720  
DB 661 POFQGRIVANLTYTLQDGHRTRRGLFPGGRHRLRNIATTSMSCTDFSFPFVQVD 720  
QY 721 LISPIVSLNFSLWEEBGTPRDQRAQKDIPIILRPSLHSETWEIPEKNGGEBKCEAN 780  
DB 721 LISPIVSLNFSLWEEBGTPRDQRAQKDIPIILRPSLHSETWEIPEKNGGEBKCEAN 780  
QY 781 LRVSPSPARSRALRLTAPASISVELSLSNLEBDAYWOLDLHPPGGLSFRVEMLKPHSQ 840  
DB 781 LRVSPSPARSRALRLTAPASISVELSLSNLEBDAYWOLDLHPPGGLSFRVEMLKPHSQ 840  
QY 841 IPVSCBELPESRRLSRALSCNVSSPIFKAGSHVALQMFENTLVNSSMGDSVELHANVC 900  
DB 841 IPVSCBELPESRRLSRALSCNVSSPIFKAGSHVALQMFENTLVNSSMGDSVELHANVC 900  
QY 901 NNEBSDLLEDNSATTIIPILYPINILIQDEBDSLTVSFTPKPKIHQVKMYQVRIOPS 960  
DB 901 NNEBSDLLEDNSATTIIPILYPINILIQDEBDSLTVSFTPKPKIHQVKMYQVRIOPS 960  
QY 961 IHDNIPITLNAVGVPOPSPSGPTTHQWSVQMEPPVCHYEDLERLPDAAPCLPGLAFR 1020  
DB 961 IHDNIPITLNAVGVPOPSPSGPTTHQWSVQMEPPVCHYEDLERLPDAAPCLPGLAFR 1020  
QY 1021 CPVYPROBIIIVOVITGLVEIEIASMSFSCSSISISFNSSKHPLVGSNLSLAQVVMK 1080  
DB 1021 CPVYPROBIIIVOVITGLVEIEIASMSFSCSSISISFNSSKHPLVGSNLSLAQVVMK 1080  
QY 1081 VDVIYKQMLLYVLSGIGGLLLILLIPIVLYKVFGRNLEKMEAGRGVPMGIPADS 1140  
DB 1081 VDVIYKQMLLYVLSGIGGLLLILLIPIVLYKVFGRNLEKMEAGRGVPMGIPADS 1140  
QY 1141 EQLASGQAGDPGCLKPLHEKDSGSGKD 1170  
DB 1141 EQLASGQAGDPGCLKPLHEKDSGSGKD 1170

RESULT 3  
US-09-945-265-2

Sequence 2, Application US/09945265  
GENERAL INFORMATION:  
APPLICANT: Springer, Timothy A.  
APPLICANT: Shimoda, Motomu  
TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A  
FILE REFERENCE: CBN-002CP  
CURRENT APPLICATION NUMBER: US/09/945,265  
PRIOR FILING DATE: 2001-08-31  
PRIOR APPLICATION NUMBER: US 60/229,700  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 1170  
TYPE: PRT

ORGANISM: Homo sapiens  
US-09-945-265-2

Query Match 100.0%; Score 6106; DB 24; Length 1170;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKSCITVMMALLSGFFPAPASSVNLVDRGASFSPPRAGRFRVLYQVNGVYGA 60  
DB 1 MKSCITVMMALLSGFFPAPASSVNLVDRGASFSPPRAGRFRVLYQVNGVYGA 60  
QY 61 PGBNATSGSLYQCGSGHCLPTVLRGSNTSKYIGMTLATDPDGSILACDPGLSTCD 120  
DB 61 PGBNATSGSLYQCGSGHCLPTVLRGSNTSKYIGMTLATDPDGSILACDPGLSTCD 120  
QY 121 QNTYLSGLCYLFRONTQGPMLQGRPGFOECIKGNVDLVFLPDGMSLQDEFOKILDFMK 180  
DB 121 QNTYLSGLCYLFRONTQGPMLQGRPGFOECIKGNVDLVFLPDGMSLQDEFOKILDFMK 180  
QY 181 DVMKLSNTSYQFAAVOPSTSYKTEPDSYVYKRPDALLKHYKMLLTNTFGALNV 240  
DB 181 DVMKLSNTSYQFAAVOPSTSYKTEPDSYVYKRPDALLKHYKMLLTNTFGALNV 240  
QY 241 ATEVFRBELGARPATYKVLIIITDGEATDSGNIDAAKDIIRYIIGIKHFQTKESQETIH 300  
DB 241 ATEVFRBELGARPATYKVLIIITDGEATDSGNIDAAKDIIRYIIGIKHFQTKESQETIH 300  
QY 301 KFAKSPASEFYKIDTFEKLKDLFTLEOKKIYIEGTSKODLTSFNNELSSSGISADLSR 360  
DB 301 KFAKSPASEFYKIDTFEKLKDLFTLEOKKIYIEGTSKODLTSFNNELSSSGISADLSR 360  
QY 361 GHAVVAGVAKDWAAGFLDKADLQDDTFIGNEBPLTEVRAGYGYVTMLPSQKTSLL 420  
DB 361 GHAVVAGVAKDWAAGFLDKADLQDDTFIGNEBPLTEVRAGYGYVTMLPSQKTSLL 420  
QY 421 ASGAPRYOHMGRVLLFQEPQGGHMSQVOTIHGQISYFGGELCGVVDODGETELLII 480  
DB 421 ASGAPRYOHMGRVLLFQEPQGGHMSQVOTIHGQISYFGGELCGVVDODGETELLII 480  
QY 481 GAPLFYEGORGRVFIYQRRQLGFEEVSELQDPEYPLGRGFEATLTALTDINGDLVDA 540  
DB 481 GAPLFYEGORGRVFIYQRRQLGFEEVSELQDPEYPLGRGFEATLTALTDINGDLVDA 540  
QY 541 VGAPLEEQGAVYIFNGRHGGLSPQSPQRIEGTQVLSGIQWFGRSIHGVKDLBGDLADVA 600  
DB 541 VGAPLEEQGAVYIFNGRHGGLSPQSPQRIEGTQVLSGIQWFGRSIHGVKDLBGDLADVA 600  
QY 601 VGASQOMIVLSSRPVDMVTLMSPFPAIPVHEVECSYSTSNKKEGVNITICQIKSLY 660  
DB 601 VGASQOMIVLSSRPVDMVTLMSPFPAIPVHEVECSYSTSNKKEGVNITICQIKSLY 660  
QY 661 POFQGRIVANLTYTLQDGHRTRRGLFPGGRHRLRNIATTSMSCTDFSFPFVQVD 720  
DB 661 POFQGRIVANLTYTLQDGHRTRRGLFPGGRHRLRNIATTSMSCTDFSFPFVQVD 720  
QY 721 LISPIVSLNFSLWEEBGTPRDQRAQKDIPIILRPSLHSETWEIPEKNGGEBKCEAN 780  
DB 721 LISPIVSLNFSLWEEBGTPRDQRAQKDIPIILRPSLHSETWEIPEKNGGEBKCEAN 780  
QY 781 LRVSPSPARSRALRLTAPASISVELSLSNLEBDAYWOLDLHPPGGLSFRVEMLKPHSQ 840  
DB 781 LRVSPSPARSRALRLTAPASISVELSLSNLEBDAYWOLDLHPPGGLSFRVEMLKPHSQ 840  
QY 841 IPVSCBELPESRRLSRALSCNVSSPIFKAGSHVALQMFENTLVNSSMGDSVELHANVC 900  
DB 841 IPVSCBELPESRRLSRALSCNVSSPIFKAGSHVALQMFENTLVNSSMGDSVELHANVC 900  
QY 901 NNEBSDLLEDNSATTIIPILYPINILIQDEBDSLTVSFTPKPKIHQVKMYQVRIOPS 960  
DB 901 NNEBSDLLEDNSATTIIPILYPINILIQDEBDSLTVSFTPKPKIHQVKMYQVRIOPS 960  
QY 961 IHDNIPITLNAVGVPOPSPSGPTTHQWSVQMEPPVCHYEDLERLPDAAPCLPGLAFR 1020  
DB 961 IHDNIPITLNAVGVPOPSPSGPTTHQWSVQMEPPVCHYEDLERLPDAAPCLPGLAFR 1020

Db 961 IHENIPTLEAVGVGPSPBSGPIITHQWSVOMEPPVPCHEDELERLPPDAAPCLJGALFR 1020  
Qy 1021 CPVVEROEILVQVIGTLELVEGEIEASSMFSLCSSLSISFNSSKPHFLYGSNASTLAQVYMK 1080  
Db 1021 CPVVEROEILVQVIGTLELVEGEIEASSMFSLCSSLSISFNSSKPHFLYGSNASTLAQVYMK 1080  
Qy 1081 VDVIYERKQMLYLYVLSIGIGILLLLIFIVLYKVGFFKRNKKEKMEAGRGVNGIPADS 1140  
Db 1081 VDVIYERKQMLYLYVLSIGIGILLLLIFIVLYKVGFFKRNKKEKMEAGRGVNGIPADS 1140  
Qy 1141 EQLASGQADPGCLKPLHKKDSBSGGKD 1170  
Db 1141 EQLASGQADPGCLKPLHKKDSBSGGKD 1170

## RESULT 4

US-10-473-127-1743  
; Sequence 1743, Application US/10473127  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; PRIOR FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1743  
; LENGTH: 1170  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-473-127-1743

Query Match 100.0%; Score 6106; DB 30; Length 1170;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKDSCITVAMAMALLSGFFFPASSYNLDVGRARSFSPRAGRHRFGYRVLQVNGVIVGA 60  
Db 1 MKDSCITVAMAMALLSGFFFPASSYNLDVGRARSFSPRAGRHRFGYRVLQVNGVIVGA 60  
Qy 61 PGEKNTSTSLYQCGSGTGHCLPVTIRGNTSKYIGMTLADPTDGSILACDPGLSRCTD 120  
Db 61 PGEKNTSTSLYQCGSGTGHCLPVTIRGNTSKYIGMTLADPTDGSILACDPGLSRCTD 120  
Qy 121 QNTYLSGLCYFRQMLQGPMLQGRPGFOEJIKANVDLFLFDGSMSLPDEROKLIDFMK 180  
Db 121 QNTYLSGLCYFRQMLQGPMLQGRPGFOEJIKANVDLFLFDGSMSLPDEROKLIDFMK 180  
Qy 181 DVMKGLSTSYQFAAVQSTSYKTEFSDYVKRDPDALLKHYVGMMLTNTFGAINVY 240  
Db 181 DVMKGLSTSYQFAAVQSTSYKTEFSDYVKRDPDALLKHYVGMMLTNTFGAINVY 240  
Qy 241 ATEVFRRELGARPDATKVLIIITDGEARDSGNIDAAKIIRIYIGIGHFQTKESQETLH 300  
Db 241 ATEVFRRELGARPDATKVLIIITDGEARDSGNIDAAKIIRIYIGIGHFQTKESQETLH 300  
Qy 301 KFAASKPASEFVKILDTFEKLDLFTLQKXIYVIGTSKODLTSFNMELSSSGISADLSR 360  
Db 301 KFAASKPASEFVKILDTFEKLDLFTLQKXIYVIGTSKODLTSFNMELSSSGISADLSR 360  
Qy 361 GHAAVAVGAKDWMAGFLDLKADLQDDTFIGNEPILPEVRAGVLYGYVTWLPSPKQTSLL 420

Db 361 GHAAVAVGAKDWMAGFLDLKADLQDDTFIGNEPILPEVRAGVLYGYVTWLPSPKQTSLL 420  
Qy 421 ASGAPRYOHMGRVTLROEPQGGHWSOVOTIHQVIGSYGSELGCVUDVODGETELLII 480  
Db 421 ASGAPRYOHMGRVTLROEPQGGHWSOVOTIHQVIGSYGSELGCVUDVODGETELLII 480  
Qy 481 GAPLFYGEORGGRVFIYQRQLGFEESVSELQSPGYLGRFGAETALTIDINGGLVDVA 540  
Db 481 GAPLFYGEORGGRVFIYQRQLGFEESVSELQSPGYLGRFGAETALTIDINGGLVDVA 540  
Qy 541 VGAPLEEQGAVYIFNGHGLSPQPSORIGTOYLSGIQMPGSHGVKDLBGDGLADVA 600  
Db 541 VGAPLEEQGAVYIFNGHGLSPQPSORIGTOYLSGIQMPGSHGVKDLBGDGLADVA 600  
Qy 601 VGAESOMIVLSSRVVMQMLMSFSPAIFVHVEGCSYSTNMKECVNTTICQIKSLY 660  
Db 601 VGAESOMIVLSSRVVMQMLMSFSPAIFVHVEGCSYSTNMKECVNTTICQIKSLY 660  
Qy 661 POFQGRIVANLTYTLQDGHRTTRRGLFPGRHELRNIAVTTSMSCTDSPFHPVCVD 720  
Db 661 POFQGRIVANLTYTLQDGHRTTRRGLFPGRHELRNIAVTTSMSCTDSPFHPVCVD 720  
Qy 721 LISPINVSLNFSLWEEBGTPRDQAGKDIPILRPSLHSEIWEIPEKXCGEDKCEAN 780  
Db 721 LISPINVSLNFSLWEEBGTPRDQAGKDIPILRPSLHSEIWEIPEKXCGEDKCEAN 780  
Qy 781 LRVSFSPARBARALRTFASLSVELSTSNLEDAVWQDLHPPGISFVKVEMLKPHSQ 840  
Db 781 LRVSFSPARBARALRTFASLSVELSTSNLEDAVWQDLHPPGISFVKVEMLKPHSQ 840  
Qy 841 IPVSCEELPEESRLLSRALSCNVSPIFKAGHSVALQMFNTLVNSWGSVELHANVTC 900  
Db 841 IPVSCEELPEESRLLSRALSCNVSPIFKAGHSVALQMFNTLVNSWGSVELHANVTC 900  
Qy 901 NNEDSDILEDNASATTIIPILYINILIQODESTLYVSFTPKPKXIHQVXMTQVRIOPS 960  
Db 901 NNEDSDILEDNASATTIIPILYINILIQODESTLYVSFTPKPKXIHQVXMTQVRIOPS 960  
Qy 961 IHENIPTLEAVGVGPSPBSGPIITHQWSVOMEPPVPCHEDELERLPPDAAPCLJGALFR 1020  
Db 961 IHENIPTLEAVGVGPSPBSGPIITHQWSVOMEPPVPCHEDELERLPPDAAPCLJGALFR 1020  
Qy 1021 CPVVEROEILVQVIGTLELVEGEIEASSMFSLCSSLSISFNSSKPHFLYGSNASTLAQVYMK 1080  
Db 1021 CPVVEROEILVQVIGTLELVEGEIEASSMFSLCSSLSISFNSSKPHFLYGSNASTLAQVYMK 1080  
Qy 1081 VDVIYERKQMLYLYVLSIGIGILLLLIFIVLYKVGFFKRNKKEKMEAGRGVNGIPADS 1140  
Db 1081 VDVIYERKQMLYLYVLSIGIGILLLLIFIVLYKVGFFKRNKKEKMEAGRGVNGIPADS 1140  
Qy 1141 EQLASGQADPGCLKPLHKKDSBSGGKD 1170  
Db 1141 EQLASGQADPGCLKPLHKKDSBSGGKD 1170

## RESULT 5

PCT-US02-09671-1737  
; Sequence 1737, Application PC/TUS0209671  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: PCT/US02/09671  
; PRIOR FILING DATE: 2002-03-28  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01

```

PRIOR APPLICATION NUMBER: 60/336,780
PRIOR FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 60/358,985
PRIOR FILING DATE: 2002-02-20
NUMBER OF SEQ ID NOS: 2041
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1737
LENGTH: 1170
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-09671-1737

Query Match      99.9%; Score 6098; DB 1; Length 1170;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKDSCITVMAMALLSGFFFPAPASSYNDVGRASFPSPRAGRHHGVRVLOVNGVIVGA 60
Db 1 MKDSCITVMAMALLSGFFFPAPASSYNDVGRASFPSPRAGRHHGVRVLOVNGVIVGA 60
Qy 61 PGEKNSGSLVQCOSGTHCLPVTLRGSNTSKYLGMTLATDPTDGSILACDPGLSRTCD 120
Db 61 PGEKNSGSLVQCOSGTHCLPVTLRGSNTSKYLGMTLATDPTDGSILACDPGLSRTCD 120
Qy 121 QNTYLSGICYLFRONTLOGPMLQGRPGFQECIKGNVDLVFLFDGSMLOPDEFQKILDFMK 180
Db 121 QNTYLSGICYLFRONTLOGPMLQGRPGFQECIKGNVDLVFLFDGSMLOPDEFQKILDFMK 180
Qy 121 QNTYLSGICYLFRONTLOGPMLQGRPGFQECIKGNVDLVFLFDGSMLOPDEFQKILDFMK 180
Db 121 QNTYLSGICYLFRONTLOGPMLQGRPGFQECIKGNVDLVFLFDGSMLOPDEFQKILDFMK 180
Qy 181 DVMKCLNTSYQFAAVOSTSYKTEPDSYVKMDPALLKHVGMILLNTTGAINYV 240
Db 181 DVMKCLNTSYQFAAVOSTSYKTEPDSYVKMDPALLKHVGMILLNTTGAINYV 240
Qy 241 ATBVRREELGARPDATKYLIIITDGEATDSGNIDAADIIIRYIGIGHPQTKSQETLH 300
Db 241 ATBVRREELGARPDATKYLIIITDGEATDSGNIDAADIIIRYIGIGHPQTKSQETLH 300
Qy 301 KPAKSPASEFYKILDFEKLKDLFELOKTIYVIGTSKODLTSSNMELSSGISADLSR 360
Db 301 KPAKSPASEFYKILDFEKLKDLFELOKTIYVIGTSKODLTSSNMELSSGISADLSR 360
Qy 361 GHAUVGAVGAKDMAGFLDLRADLDDPTFIGNEPILTEPVARGVIGYTWMLPSRKTSIL 420
Db 361 GHAUVGAVGAKDMAGFLDLRADLDDPTFIGNEPILTEPVARGVIGYTWMLPSRKTSIL 420
Qy 421 ASGAPRYOHMGKRVLLFOBPQGGHMSQVQTHIGTIGSYFGGELCGVVDVDDGETELLII 480
Db 421 ASGAPRYOHMGKRVLLFOBPQGGHMSQVQTHIGTIGSYFGGELCGVVDVDDGETELLII 480
Qy 481 GAPLFYGRQGRGVITYORRQLGFEVESELQGDPEYPLGRGFEATLTALTDINGDLVVA 540
Db 481 GAPLFYGRQGRGVITYORRQLGFEVESELQGDPEYPLGRGFEATLTALTDINGDLVVA 540
Qy 541 VGAPLEEGGAVYIFNGRHGSLPOPSORIEGTVLSGIOWGGRSHGVKLEGGDLADVA 600
Db 541 VGAPLEEGGAVYIFNGRHGSLPOPSORIEGTVLSGIOWGGRSHGVKLEGGDLADVA 600
Qy 601 VGASQOMIVLSSRPVDMVTILMSFSPAEI PVHEVCSYSTSNKMEGNITTCFOIKSLY 660
Db 601 VGASQOMIVLSSRPVDMVTILMSFSPAEI PVHEVCSYSTSNKMEGNITTCFOIKSLY 660
Qy 661 POPQGRIVANTLYTQLDGHRTRRRGLFGGRIHEIRNI AVTTSMSCTDPSFHPVQCQD 720
Db 661 POPQGRIVANTLYTQLDGHRTRRRGLFGGRIHEIRNI AVTTSMSCTDPSFHPVQCQD 720
Qy 721 LIISPINVSINFSIMEEGTPRDORQOGKDIPIILRPSLHSTWELPFEKNGGDDKCCAN 780
Db 721 LIISPINVSINFSIMEEGTPRDORQOGKDIPIILRPSLHSTWELPFEKNGGDDKCCAN 780
Qy 781 LRVSPSPARSLRLTAFASLSVELSLSNLEBEDAYVOLDLHFPGLSFRKVEMLKPSHQ 840
Db 781 LRVSPSPARSLRLTAFASLSVELSLSNLEBEDAYVOLDLHFPGLSFRKVEMLKPSHQ 840
Qy 841 IPVSCBELPERSRLSRALSCNVSSPIFKAGHSVALQMMFNTLVNNSMGDSVELHANVTC 900

```

```

841 IPVSCBELPERSRLSRALSCNVSSPIFKAGHSVALQMMFNTLVNNSMGDSVELHANVTC 900
901 NNEBDDLEDNSATTIPIIYPINILLIQDEDSLYVSFTPKGPKIHQVKMYQVRIOPS 960
901 NNEBDDLEDNSATTIPIIYPINILLIQDEDSLYVSFTPKGPKIHQVKMYQVRIOPS 960
961 IHDNITPLEAVGVVPPSPSGRPTTHQMSVQMEPPVCHIEDLERLDDAEPCLPGLFR 1020
961 IHDNITPLEAVGVVPPSPSGRPTTHQMSVQMEPPVCHIEDLERLDDAEPCLPGLFR 1020
1021 CPVVRROBILYQVGTLELVEGEIRASSMFSLCSLSISFNSSSKHFIH XGSNASTAQQVMK 1080
1021 CPVVRROBILYQVGTLELVEGEIRASSMFSLCSLSISFNSSSKHFIH XGSNASTAQQVMK 1080
1081 VDVIYKQMLYLYLSGIGILLILLIFLYLKYKGFERNLKEKMEAGRGVPNGIPADS 1140
1081 VDVIYKQMLYLYLSGIGILLILLIFLYLKYKGFERNLKEKMEAGRGVPNGIPADS 1140
1141 EQLASQAGDPGCLKPLHEDSBSGGKD 1170
1141 EQLASQAGDPGCLKPLHEDSBSGGKD 1170

RESULT 6
PCT-US02-09671-1739
Sequence 1739, Application PC/TUS0209671
GENERAL INFORMATION:
APPLICANT: Zycos Inc.
TITLE OF INVENTION: TRANSLATIONAL PROFILING
FILE REFERENCE: 08191-026W01
CURRENT APPLICATION NUMBER: PCT/US02/09671
PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: 60/279,495
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: 60/292,544
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 60/310,801
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/326,370
PRIOR FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: 60/336,780
PRIOR FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 60/358,985
PRIOR FILING DATE: 2002-02-20
NUMBER OF SEQ ID NOS: 2041
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1739
LENGTH: 1170
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-09671-1739

Query Match      99.9%; Score 6098; DB 1; Length 1170;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKDSCITVMAMALLSGFFFPAPASSYNDVGRASFPSPRAGRHHGVRVLOVNGVIVGA 60
Db 1 MKDSCITVMAMALLSGFFFPAPASSYNDVGRASFPSPRAGRHHGVRVLOVNGVIVGA 60
Qy 61 PGEKNSGSLVQCOSGTHCLPVTLRGSNTSKYLGMTLATDPTDGSILACDPGLSRTCD 120
Db 61 PGEKNSGSLVQCOSGTHCLPVTLRGSNTSKYLGMTLATDPTDGSILACDPGLSRTCD 120
Qy 121 QNTYLSGICYLFRONTLOGPMLQGRPGFQECIKGNVDLVFLFDGSMLOPDEFQKILDFMK 180
Db 121 QNTYLSGICYLFRONTLOGPMLQGRPGFQECIKGNVDLVFLFDGSMLOPDEFQKILDFMK 180
Qy 181 DVMKCLNTSYQFAAVOSTSYKTEPDSYVKMDPALLKHVGMILLNTTGAINYV 240
Db 181 DVMKCLNTSYQFAAVOSTSYKTEPDSYVKMDPALLKHVGMILLNTTGAINYV 240

```

```
Qy 241 ATEVFREELGARPDATKVLIIITDGEATDSGNIDAADKIIRYIIIGIGHFQTKESQETLH 300
Db 241 ATEVFREELGARPDATKVLIIITDGEATDSGNIDAADKIIRYIIIGIGHFQTKESQETLH 300
Qy 301 KFAKSPASEFVKIIDLTEFKLKDLPTELQKTIYVIEGTSKODLTSFNNELSSSGISADLSR 360
Db 301 KFAKSPASEFVKIIDLTEFKLKDLPTELQKTIYVIEGTSKODLTSFNNELSSSGISADLSR 360
Qy 361 GHAVVAGAKDMAGGFLDLKADLQDDTFIGNEPILPEVRAGYLGVTWMLPSRQKTSLL 420
Db 361 GHAVVAGAKDMAGGFLDLKADLQDDTFIGNEPILPEVRAGYLGVTWMLPSRQKTSLL 420
Qy 421 ASGAPRYOHMGKRVLLFQEPQGGHMSQVQTIHGTOIGSYFGGELCGVDVDDQGETELLII 480
Db 421 ASGAPRYOHMGKRVLLFQEPQGGHMSQVQTIHGTOIGSYFGGELCGVDVDDQGETELLII 480
Qy 481 GAPLFYEGORGRVFIYQRRQLGFEVSELOQDPGYLGRGEGALITALTINDGGLADVA 540
Db 481 GAPLFYEGORGRVFIYQRRQLGFEVSELOQDPGYLGRGEGALITALTINDGGLADVA 540
Qy 541 VGAPLEBQAGVYIFNGRHGGLSPQSORIEGTQVLSGIQWFGRSIHGVKDLBEGDLADVA 600
Db 541 VGAPLEBQAGVYIFNGRHGGLSPQSORIEGTQVLSGIQWFGRSIHGVKDLBEGDLADVA 600
Qy 601 VQASQOMIVLSSRPVDMVTLMSPAPAI PVHEVBCSYSTSNKMEGVNITTCQIKSLY 660
Db 601 VQASQOMIVLSSRPVDMVTLMSPAPAI PVHEVBCSYSTSNKMEGVNITTCQIKSLY 660
Qy 661 POFQGRIVANULTYTLQDGHRTTRRGLFPGGRHELRNIAVTTSMSCITDSEFHPVCVOD 720
Db 661 POFQGRIVANULTYTLQDGHRTTRRGLFPGGRHELRNIAVTTSMSCITDSEFHPVCVOD 720
Qy 721 LISPIVNSLANSMEEBGTPRDQAOQKDIPIILPSLHSETWELPEFKNGCEDKKCEAN 780
Db 721 LISPIVNSLANSMEEBGTPRDQAOQKDIPIILPSLHSETWELPEFKNGCEDKKCEAN 780
Qy 781 LRVSPSPARSALRLTAPASLSVELSLNEBEDAVWQDLHFPPGLSFRKVEMLKPHSQ 840
Db 781 LRVSPSPARSALRLTAPASLSVELSLNEBEDAVWQDLHFPPGLSFRKVEMLKPHSQ 840
Qy 841 IPVSCBELPEBSRLISRLSCNVSSPIFKAGHSVALQMMFNTLVNSSGSDSEVELHANTYC 900
Db 841 IPVSCBELPEBSRLISRLSCNVSSPIFKAGHSVALQMMFNTLVNSSGSDSEVELHANTYC 900
Qy 901 NNEBSDLLEDNSATTIPIILPINILIODOSDTLYSFTPKGPIKHQVKMYOVRLOPS 960
Db 901 NNEBSDLLEDNSATTIPIILPINILIODOSDTLYSFTPKGPIKHQVKMYOVRLOPS 960
Qy 961 IHDNRIPTLEAVGVPOPSBGPITHQMSVQMEBPVPCHEYDLERLPDAEPCLPGALFR 1020
Db 961 IHDNRIPTLEAVGVPOPSBGPITHQMSVQMEBPVPCHEYDLERLPDAEPCLPGALFR 1020
Qy 1021 CPVYFRQGIILVOYIGTLELVGEIEASMSFSLCSSISIFNSSKIFHLXGSAJLAQVVMK 1080
Db 1021 CPVYFRQGIILVOYIGTLELVGEIEASMSFSLCSSISIFNSSKIFHLXGSAJLAQVVMK 1080
Qy 1081 DVVYVEKQMLYLYLSGIGLLLLLIPIYLXKVGFPKRNKEKKEAGRGVNGIPARDS 1140
Db 1081 DVVYVEKQMLYLYLSGIGLLLLLIPIYLXKVGFPKRNKEKKEAGRGVNGIPARDS 1140
Qy 1141 EQLASGEAGDPGCLKPLHEKDSBGGKXD 1170
Db 1141 EQLASGEAGDPGCLKPLHEKDSBGGKXD 1170
```

RESULT 7  
PCT-US02-09671-1742  
; Sequence 1742, Application PC/TUS0209671  
; GENERAL INFORMATION:

; APPLICANT: Zycoos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026WO1  
; CURRENT APPLICATION NUMBER: PCT/US02/09671

```
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1742
; LENGTH: 1170
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-09671-1742
```

Query Match 99.9%; Score 6098; DB 1; Length 1170;

Best Local Similarity 99.9%; Pred. No. 0; Matches 1169; Mismatches 1; Indels 0; Gaps 0;

```
Qy 1 MKDSCTIVMAMALISGFFFPAPASSYNLVDRGARSFSPRAGRHFGYRVLOVANGVYGA 60
Db 1 MKDSCTIVMAMALISGFFFPAPASSYNLVDRGARSFSPRAGRHFGYRVLOVANGVYGA 60
Qy 61 PGBGNSYSGSLYQCSGTHGCLPVTLRGSNTSKYLGMTLATDPTDGSIIACDPGLSRTCD 120
Db 61 PGBGNSYSGSLYQCSGTHGCLPVTLRGSNTSKYLGMTLATDPTDGSIIACDPGLSRTCD 120
Qy 121 QNTYLSGLCYLFRQNLQCPMLQGRPGROBCKGNVULVFLPDSMSIQPDEFQKILDFMK 180
Db 121 QNTYLSGLCYLFRQNLQCPMLQGRPGROBCKGNVULVFLPDSMSIQPDEFQKILDFMK 180
Qy 181 DVMKLSNTSYQFAAVQFSTSYKTEPFSQDYVRKQPDALLKHYKMLLTNTFGAINTV 240
Db 181 DVMKLSNTSYQFAAVQFSTSYKTEPFSQDYVRKQPDALLKHYKMLLTNTFGAINTV 240
Qy 241 ATEVFREELGARPDATKVLIIITDGEATDSGNIDAADKIIRYIIIGIGHFQTKESQETLH 300
Db 241 ATEVFREELGARPDATKVLIIITDGEATDSGNIDAADKIIRYIIIGIGHFQTKESQETLH 300
Qy 301 KFAKSPASEFVKIIDLTEFKLKDLPTELQKTIYVIEGTSKODLTSFNNELSSSGISADLSR 360
Db 301 KFAKSPASEFVKIIDLTEFKLKDLPTELQKTIYVIEGTSKODLTSFNNELSSSGISADLSR 360
Qy 361 GHAVVAGAKDMAGGFLDLKADLQDDTFIGNEPILPEVRAGYLGVTWMLPSRQKTSLL 420
Db 361 GHAVVAGAKDMAGGFLDLKADLQDDTFIGNEPILPEVRAGYLGVTWMLPSRQKTSLL 420
Qy 421 ASGAPRYOHMGKRVLLFQEPQGGHMSQVQTIHGTOIGSYFGGELCGVDVDDQGETELLII 480
Db 421 ASGAPRYOHMGKRVLLFQEPQGGHMSQVQTIHGTOIGSYFGGELCGVDVDDQGETELLII 480
Qy 481 GAPLFYEGORGRVFIYQRRQLGFEVSELOQDPGYLGRGEGALITALTINDGGLADVA 540
Db 481 GAPLFYEGORGRVFIYQRRQLGFEVSELOQDPGYLGRGEGALITALTINDGGLADVA 540
Qy 541 VGAPLEBQAGVYIFNGRHGGLSPQSORIEGTQVLSGIQWFGRSIHGVKDLBEGDLADVA 600
Db 541 VGAPLEBQAGVYIFNGRHGGLSPQSORIEGTQVLSGIQWFGRSIHGVKDLBEGDLADVA 600
Qy 601 VQASQOMIVLSSRPVDMVTLMSPAPAI PVHEVBCSYSTSNKMEGVNITTCQIKSLY 660
Db 601 VQASQOMIVLSSRPVDMVTLMSPAPAI PVHEVBCSYSTSNKMEGVNITTCQIKSLY 660
Qy 661 POFQGRIVANULTYTLQDGHRTTRRGLFPGGRHELRNIAVTTSMSCITDSEFHPVCVOD 720
Db 661 POFQGRIVANULTYTLQDGHRTTRRGLFPGGRHELRNIAVTTSMSCITDSEFHPVCVOD 720
```



Qy	721	LI\$PI\$NV\$LN\$T\$LM\$W\$E\$B\$T\$P\$P\$D\$O\$R\$O\$G\$D\$I\$P\$II\$A\$P\$S\$H\$S\$E\$T\$W\$E\$I\$P\$P\$E\$K\$N\$G\$E\$D\$K\$K\$C\$E\$A\$N	780
Db	721	LIS\$PI\$NV\$LN\$T\$LM\$W\$E\$B\$T\$P\$P\$D\$O\$R\$O\$G\$D\$I\$P\$II\$A\$P\$S\$H\$S\$E\$T\$W\$E\$I\$P\$P\$E\$K\$N\$G\$E\$D\$K\$K\$C\$E\$A\$N	780
Qy	781	L\$R\$V\$S\$P\$A\$R\$S\$A\$L\$R\$T\$A\$F\$A\$S\$L\$S\$V\$E\$L\$S\$T\$N\$L\$E\$D\$A\$F\$W\$O\$L\$D\$L\$F\$P\$G\$L\$F\$R\$K\$Y\$E\$M\$L\$K\$P\$H\$S\$Q	840
Db	781	L\$R\$V\$S\$P\$A\$R\$S\$A\$L\$R\$T\$A\$F\$A\$S\$L\$S\$V\$E\$L\$S\$T\$N\$L\$E\$D\$A\$F\$W\$O\$L\$D\$L\$F\$P\$G\$L\$F\$R\$K\$Y\$E\$M\$L\$K\$P\$H\$S\$Q	840
Qy	841	I\$P\$V\$S\$C\$E\$E\$L\$P\$E\$B\$S\$R\$L\$I\$S\$R\$A\$L\$S\$C\$N\$V\$S\$E\$P\$I\$F\$A\$G\$H\$S\$V\$A\$L\$O\$M\$M\$E\$N\$T\$L\$V\$N\$S\$W\$G\$D\$S\$Y\$E\$L\$H\$A\$N\$T\$C	900
Db	841	I\$P\$V\$S\$C\$E\$E\$L\$P\$E\$B\$S\$R\$L\$I\$S\$R\$A\$L\$S\$C\$N\$V\$S\$E\$P\$I\$F\$A\$G\$H\$S\$V\$A\$L\$O\$M\$M\$E\$N\$T\$L\$V\$N\$S\$W\$G\$D\$S\$Y\$E\$L\$H\$A\$N\$T\$C	900
Qy	901	N\$N\$E\$D\$D\$L\$E\$D\$N\$S\$A\$T\$T\$I\$P\$I\$P\$Y\$P\$N\$T\$L\$I\$D\$O\$E\$S\$T\$Y\$S\$F\$T\$P\$K\$P\$K\$I\$H\$O\$V\$K\$M\$Y\$O\$V\$R\$I\$O\$P\$S	960
Db	901	N\$N\$E\$D\$D\$L\$E\$D\$N\$S\$A\$T\$T\$I\$P\$I\$P\$Y\$P\$N\$T\$L\$I\$D\$O\$E\$S\$T\$Y\$S\$F\$T\$P\$K\$P\$K\$I\$H\$O\$V\$K\$M\$Y\$O\$V\$R\$I\$O\$P\$S	960
Qy	961	I\$H\$D\$H\$I\$P\$T\$L\$E\$A\$V\$G\$V\$P\$O\$P\$P\$E\$B\$G\$P\$I\$T\$H\$O\$M\$S\$V\$O\$M\$E\$P\$P\$C\$H\$Y\$D\$E\$L\$R\$L\$P\$D\$A\$E\$B\$C\$L\$G\$A\$L\$F\$R	1020
Db	961	I\$H\$D\$H\$I\$P\$T\$L\$E\$A\$V\$G\$V\$P\$O\$P\$P\$E\$B\$G\$P\$I\$T\$H\$O\$M\$S\$V\$O\$M\$E\$P\$P\$C\$H\$Y\$D\$E\$L\$R\$L\$P\$D\$A\$E\$B\$C\$L\$G\$A\$L\$F\$R	1020
Qy	1021	C\$P\$V\$P\$R\$O\$E\$L\$I\$V\$O\$G\$T\$L\$E\$F\$L\$V\$G\$I\$E\$A\$S\$M\$F\$S\$L\$C\$S\$S\$I\$S\$T\$S\$F\$N\$S\$K\$H\$H\$Y\$L\$G\$S\$N\$A\$S\$L\$A\$Q\$V\$M\$K	1080
Db	1021	C\$P\$V\$P\$R\$O\$E\$L\$I\$V\$O\$G\$T\$L\$E\$F\$L\$V\$G\$I\$E\$A\$S\$M\$F\$S\$L\$C\$S\$S\$I\$S\$T\$S\$F\$N\$S\$K\$H\$H\$Y\$L\$G\$S\$N\$A\$S\$L\$A\$Q\$V\$M\$K	1080
Qy	1081	V\$D\$V\$V\$E\$K\$O\$M\$L\$Y\$L\$Y\$V\$S\$G\$I\$G\$G\$L\$L\$L\$L\$L\$L\$I\$F\$I\$V\$Y\$K\$V\$F\$F\$R\$N\$L\$E\$K\$K\$E\$A\$G\$R\$G\$V\$P\$N\$G\$I\$P\$A\$D\$S	1140
Db	1081	V\$D\$V\$V\$E\$K\$O\$M\$L\$Y\$L\$Y\$V\$S\$G\$I\$G\$G\$L\$L\$L\$L\$L\$L\$I\$F\$I\$V\$Y\$K\$V\$F\$F\$R\$N\$L\$E\$K\$K\$E\$A\$G\$R\$G\$V\$P\$N\$G\$I\$P\$A\$D\$S	1140
Qy	1141	E\$Q\$L\$A\$S\$G\$O\$A\$G\$D\$P\$G\$C\$L\$K\$P\$L\$H\$E\$K\$D\$S\$E\$G\$G\$K\$D	1170
Db	1141	E\$Q\$L\$A\$S\$G\$O\$A\$G\$D\$P\$G\$C\$L\$K\$P\$L\$H\$E\$K\$D\$S\$E\$G\$G\$K\$D	1170

```

RESULT 8
PCT-US03-12946-3007
; Sequence 3007, Application PC/TUS0312946
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000150
; CURRENT APPLICATION NUMBER: PCT/US03/12946
; CURRENT FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,827
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3007
; LENGTH: 1170
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-12946-3007

```

Query Match	99.9%	Score 6098	DB 1	Length 1170
Query Local Similarity	99.9%	Pred No. 0		
Matches 1169	Conservative	Mismatches 1	Indels 0	Gaps 0
QY	1	MKDSCTTWMANALSGFFFPASSYINLDVGRARFSPPRAGRHRGYRLQYGNVYIGA	60	
Db	1	MKDSCTTWMANALSGFFFPASSYINLDVGRARFSPPRAGRHRGYRLQYGNVYIGA	60	
QY	61	PGEGNSTSLYOCOSGTGCHCFLVTLRGSNYSKYLGMTLATPTGSLIACDPGSLRTCD	120	
Db	61	PGEGNSTSLYOCOSGTGCHCFLVTLRGSNYSKYLGMTLATPTGSLIACDPGSLRTCD	120	

QY	121	QNTYLSGLCYLFRONTLOQPMLOQGRPGOECKXGVNDLVFLPDSMSLSQDPEFOKILDPMK	180
Db	121	QNTYLSGLCYLFRONTLOQPMLOQGRPGOECKXGVNDLVFLPDSMSLSQDPEFOKILDPMK	180
QY	181	DVMKGLNTSVOFAAVOFTSYKTEPFPSDVVKKDKDALLKRVKXNMLLTNTFGALINVY	240
Db	181	DVMKGLNTSYQFAAVOFTSYKTEPFPSDVVKKDKDALLKRVKXNMLLTNTFGALINVY	240
QY	241	ATEVFRSELGARPATKVLIIITDGEATDSGNIDAAKDIIRYIIGIKHFOTKESQETH	300
Db	241	ATEVFRSELGARPATKVLIIITDGEATDSGNIDAAKDIIRYIIGIKHFOTKESQETH	300
QY	301	KPASKPASEPVKILDTFEKLDLFELOKIKYIYEGTSKODLTSFNNELSSSGISADLSR	360
Db	301	KPASKPASEPVKILDTFEKLDLFELOKIKYIYEGTSKODLTSFNNELSSSGISADLSR	360
QY	361	GHAVVAVGAKDMAGFLDLKADLODDTFLIGNEPLTEBEVAGYGVYVWMLPSKOKSL	420
Db	361	GHAVVAVGAKDMAGFLDLKADLODDTFLIGNEPLTEBEVAGYGVYVWMLPSKOKSL	420
QY	421	ASGAPRVOHMRVLLPBOPOGGGWSOVQTIHGQISYFEGSELQGVVDODGETELL	480
Db	421	ASGAPRVOHMRVLLPBOPOGGGWSOVQTIHGQISYFEGSELQGVVDODGETELL	480
QY	481	GAPLFYGBORGRVFIYORROLGFEVYSELQGDYPLGRFGAII7ALTDINGDLVDA	540
Db	481	GAPLFYGBORGRVFIYORROLGFEVYSELQGDYPLGRFGAII7ALTDINGDLVDA	540
QY	541	VGALBEEQAGVYINGRHGGLSPSPORIBETQVLSGIQWFGRSIHGVKOLEGGGLDA	600
Db	541	VGALBEEQAGVYINGRHGGLSPSPORIBETQVLSGIQWFGRSIHGVKOLEGGGLDA	600
QY	601	VGAESOMIVLSSRPVDMVMTLMS7SPABIPHEVEGYS7SNKKKEGNITICQOISLY	660
Db	601	VGAESOMIVLSSRPVDMVMTLMS7SPABIPHEVEGYS7SNKKKEGNITICQOISLY	660
QY	661	POFGSRIVANITYLOLDGHRTRRGRFPGGRHLYBRNIAVTTSMSC7DPSFHPVCOD	720
Db	661	POFGSRIVANITYLOLDGHRTRRGRFPGGRHLYBRNIAVTTSMSC7DPSFHPVCOD	720
QY	721	LISPIVNSLNFSLMEEBGT7PRDQAOQKDIPIILRPSLHSETWEIPPEKONGEDKCEAN	780
Db	721	LISPIVNSLNFSLMEEBGT7PRDQAOQKDIPIILRPSLHSETWEIPPEKONGEDKCEAN	780
QY	781	LRVSPFSPARSALMLTAPASLVS7LSNLEBDA7YWQOLDHFP7GLSFRVEMLKPSQ	840
Db	781	LRVSPFSPARSALMLTAPASLVS7LSNLEBDA7YWQOLDHFP7GLSFRVEMLKPSQ	840
QY	841	IPVSCBELPEBSRLLS7RALSCNVS7PIFKAGH57AALQMMF7TLVNS5WGBSVELHANVC	900
Db	841	IPVSCBELPEBSRLLS7RALSCNVS7PIFKAGH57AALQMMF7TLVNS5WGBSVELHANVC	900
QY	901	NNEDSDLL7EDNSAT7IIPILY7PINILIQODED7SLVYS7FKPGK7IHQV7KMYOVR7IQPS	960
Db	901	NNEDSDLL7EDNSAT7IIPILY7PINILIQODED7SLVYS7FKPGK7IHQV7KMYOVR7IQPS	960
QY	961	IHDHNI7PLEAVGV7POP7SEB7PTTHQW57OME7PV7CH7ED7RL7DPA7E7PC7GAL7FR	1020
Db	961	IHDHNI7PLEAVGV7POP7SEB7PTTHQW57OME7PV7CH7ED7RL7DPA7E7PC7GAL7FR	1020
QY	1021	CPVVR7ROBIL7VOV7GTL7ELVGE7IAS7MFS7CS7LS7SPN57KH7FHL7YGS7A57LAQ7VVMK	1080
Db	1021	CPVVR7ROBIL7VOV7GTL7ELVGE7IAS7MFS7CS7LS7SPN57KH7FHL7YGS7A57LAQ7VVMK	1080
QY	1081	VDVY7EKQML7LYV7LSG7IG7LL7LL7L7I7YL7YK7G7FKR7ML7KEM7BA7GR7V7NG7IPADS	1140
Db	1081	VDVY7EKQML7LYV7LSG7IG7LL7LL7L7I7YL7YK7G7FKR7ML7KEM7BA7GR7V7NG7IPADS	1140
QY	1141	EOLASQO7EAD7PGL7K7L7PHEKDS7SGG7KD	1170
Db	1141	EOLASQO7EAD7PGL7K7L7PHEKDS7SGG7KD	1170

Db	1021	CPVAFROELIYVIGTIELVGEIRASNSMFSICSLISFNSSKHFALYGSNALSIAQVVMK	1080
QY	1081	VDVYVEROMLYLVYLSGIGGLLLLLLI.FIYLKYKGFPERKLIKEMBAAGVPGNIPADS	1140
Db	1081	VDVYVEROMLYLVYLSGIGGLLLLLLI.FIYLKYKGFPERKLIKEMBAAGVPGNIPADS	1140
QY	1141	EQLASGGAEADPGCTKPLHEKDSSSGGKGD	1170
Db	1141	EQLASGGAEADPGCTKPLHEKDSSSGGKGD	1170

RESULT 9  
PCT-US03-40978-1088  
; Sequence 1088, Application PC/TUS0340978  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; FILE REFERENCE: CLO01499 MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF  
; CURRENT FILING DATE: 2003-12-22 PCT/US03/40978  
; NUMBER OF SEQ ID NOS: 73997  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1088  
; LENGTH: 1170  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US03-40978-1088

Query Match 99.9%; Score 6098; DB 1; Length 1170;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Oy 1 MKDSCITVMAMALLSGFFFPAPASSYNLDVRGARSFSPPRAGRHFGYRVLOVANGVYGA 60
Db 1 MKDSCITVMAMALLSGFFFPAPASSYNLDVRGARSFSPPRAGRHFGYRVLOVANGVYGA 60
Oy 61 PGBGNSGSLYOCOSGTGHCPLVTLRGSNTSKYLGMTLATDPTDGSILACDPGLSTCD 120
Db 61 PGBGNSGSLYOCOSGTGHCPLVTLRGSNTSKYLGMTLATDPTDGSILACDPGLSTCD 120
Oy 121 QNTYLSGLCYLFRONLOGPMLQGRPGFQECIKGNVDLVFLFDGSMSLQDPDEFQKILDFMK 180
Db 121 QNTYLSGLCYLFRONLOGPMLQGRPGFQECIKGNVDLVFLFDGSMSLQDPDEFQKILDFMK 180
Oy 181 DVMKLSTSYQPAAVQSTSYKTEFDFSDYKRRDPALLKHYKMLLINTFGAINVY 240
Db 181 DVMKLSTSYQPAAVQSTSYKTEFDFSDYKRRDPALLKHYKMLLINTFGAINVY 240
Oy 241 ATEVREBELGARPRATKYLIIITGEATDSGNIDAAKIIIVYIGIGKPGTKSQETLH 300
Db 241 ATEVREBELGARPRATKYLIIITGEATDSGNIDAAKIIIVYIGIGKPGTKSQETLH 300
Oy 301 KFAKSPASEFYKILDTFEKLDLFTLOKTIYIEGTSKODLTSFNMELSSSGISADLSR 360
Db 301 KFAKSPASEFYKILDTFEKLDLFTLOKTIYIEGTSKODLTSFNMELSSSGISADLSR 360
Oy 361 GHAVVGAAGVADWAGGFLDLKADLQDDTFIGNEPITPEVRAGYIGYIVTWLPSRQKISL 420
Db 361 GHAVVGAAGVADWAGGFLDLKADLQDDTFIGNEPITPEVRAGYIGYIVTWLPSRQKISL 420
Oy 421 ASGARVYOHMRGVLLFQEPQGGHMSQVQTHGTQIGSYFGGELCGVVDVDDGETELLII 480
Db 421 ASGARVYOHMRGVLLFQEPQGGHMSQVQTHGTQIGSYFGGELCGVVDVDDGETELLII 480
Oy 481 GAPLFYGGORGRVYIYORROLGFEEVSELQDPEYPIGRFGEATLTALTDINGDLVVA 540
Db 481 GAPLFYGGORGRVYIYORROLGFEEVSELQDPEYPIGRFGEATLTALTDINGDLVVA 540
Oy 541 VGAPLEEGQAVYIFNGRHGGLSPQPSQRIEGTVLSGIQWFGRSIHGVKDLBGDLADVA 600
Db 541 VGAPLEEGQAVYIFNGRHGGLSPQPSQRIEGTVLSGIQWFGRSIHGVKDLBGDLADVA 600
Oy 601 VGASQMTVLSRPPVMDVTLMSFPAIPVHEVCSYSTSNKMEGVNITICPOIKSLI 660
Db 601 VGASQMTVLSRPPVMDVTLMSFPAIPVHEVCSYSTSNKMEGVNITICPOIKSLI 660
Oy 661 POFQGRVANTLYTLQDLGHRTRRGLPPGGRHELRRIAVTTSMSCTDFSHPVVCOD 720
Db 661 POFQGRVANTLYTLQDLGHRTRRGLPPGGRHELRRIAVTTSMSCTDFSHPVVCOD 720
Oy 721 LISPIVNSLNFSLWEEGTPRDQAGKDIPIILRSLHSETWEIPPEKNCGEDKCEAN 780
Db 721 LISPIVNSLNFSLWEEGTPRDQAGKDIPIILRSLHSETWEIPPEKNCGEDKCEAN 780

```

```

Db 721 LISPIVNSLNFSLWEEGTPRDQAGKDIPIILRSLHSETWEIPPEKNCGEDKCEAN 780
Oy 781 LRVSPARARALRLTAPASLSVEILSLNLEBDAVWQULHPPGSLPRKVENTLKPESQ 840
Db 781 LRVSPARARALRLTAPASLSVEILSLNLEBDAVWQULHPPGSLPRKVENTLKPESQ 840
Oy 841 IVPSCBELPESRRLSRLSCVNSSPIFKAGHSVALQMMENTLVNSWGDSEVLIHANVTC 900
Db 841 IVPSCBELPESRRLSRLSCVNSSPIFKAGHSVALQMMENTLVNSWGDSEVLIHANVTC 900
Oy 901 NNEBSDLLEBNSATTIIPILYPINILIQODEDSTLYSFPKPKKHQYKMTQVRQPS 960
Db 901 NNEBSDLLEBNSATTIIPILYPINILIQODEDSTLYSFPKPKKHQYKMTQVRQPS 960
Oy 961 IHDNIPITLNAVGVPOPSEGPITTHQMSQVMEBPVCHVEDLRLPDAEPCPGALFR 1020
Db 961 IHDNIPITLNAVGVPOPSEGPITTHQMSQVMEBPVCHVEDLRLPDAEPCPGALFR 1020
Oy 1021 CPVVFROEILVOVIGTLELVGEIEASSMPSLCSLSISFNSKHFHLYGSNASIAQVVMK 1080
Db 1021 CPVVFROEILVOVIGTLELVGEIEASSMPSLCSLSISFNSKHFHLYGSNASIAQVVMK 1080
Oy 1081 VDVYERQMTLYLTLGIGLLILLIFLYLYKVGFFKRLKEMKAGRGVPPNGIPAEBS 1140
Db 1081 VDVYERQMTLYLTLGIGLLILLIFLYLYKVGFFKRLKEMKAGRGVPPNGIPAEBS 1140
Oy 1141 EQLASGOEAGDPGLKPLHKDSSESQSKD 1170
Db 1141 EQLASGOEAGDPGLKPLHKDSSESQSKD 1170

```

RESULT 10  
US-09-592-617A-42  
; Sequence 42, Application US/09592617A  
; GENERAL INFORMATION:  
; APPLICANT: Airtaout, M. Armin  
; TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN ANTAGONISTS  
; FILE REFERENCE: 00786-267002  
; CURRENT FILING DATE: US/09/592,617A  
; PRIOR FILING DATE: 2000-06-13  
; PRIOR APPLICATION NUMBER: US 08/380,167  
; PRIOR FILING DATE: 1999-01-30  
; PRIOR APPLICATION NUMBER: US 08/216,081  
; PRIOR FILING DATE: 1994-03-21  
; PRIOR APPLICATION NUMBER: US 07/637,830  
; PRIOR FILING DATE: 1991-01-04  
; PRIOR APPLICATION NUMBER: US 07/539,842  
; PRIOR FILING DATE: 1990-06-18  
; PRIOR APPLICATION NUMBER: US 07/212,573  
; PRIOR FILING DATE: 1988-06-28  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 42  
; LENGTH: 1170  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-592-617A-42

Query Match 99.9%; Score 6098; DB 19; Length 1170;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Oy 1 MKDSCITVMAMALLSGFFFPAPASSYNLDVRGARSFSPPRAGRHFGYRVLOVANGVYGA 60
Db 1 MKDSCITVMAMALLSGFFFPAPASSYNLDVRGARSFSPPRAGRHFGYRVLOVANGVYGA 60
Oy 61 PGBGNSGSLYOCOSGTGHCPLVTLRGSNTSKYLGMTLATDPTDGSILACDPGLSTCD 120
Db 61 PGBGNSGSLYOCOSGTGHCPLVTLRGSNTSKYLGMTLATDPTDGSILACDPGLSTCD 120
Oy 121 QNTYLSGLCYLFRONLOGPMLQGRPGFQECIKGNVDLVFLFDGSMSLQDPDEFQKILDFMK 180
Db 121 QNTYLSGLCYLFRONLOGPMLQGRPGFQECIKGNVDLVFLFDGSMSLQDPDEFQKILDFMK 180
Oy 181 DVMKLSTSYQPAAVQSTSYKTEFDFSDYKRRDPALLKHYKMLLINTFGAINVY 240
Db 181 DVMKLSTSYQPAAVQSTSYKTEFDFSDYKRRDPALLKHYKMLLINTFGAINVY 240
Oy 241 ATEVREBELGARPRATKYLIIITGEATDSGNIDAAKIIIVYIGIGKPGTKSQETLH 300
Db 241 ATEVREBELGARPRATKYLIIITGEATDSGNIDAAKIIIVYIGIGKPGTKSQETLH 300
Oy 301 KFAKSPASEFYKILDTFEKLDLFTLOKTIYIEGTSKODLTSFNMELSSSGISADLSR 360
Db 301 KFAKSPASEFYKILDTFEKLDLFTLOKTIYIEGTSKODLTSFNMELSSSGISADLSR 360
Oy 361 GHAVVGAAGVADWAGGFLDLKADLQDDTFIGNEPITPEVRAGYIGYIVTWLPSRQKISL 420
Db 361 GHAVVGAAGVADWAGGFLDLKADLQDDTFIGNEPITPEVRAGYIGYIVTWLPSRQKISL 420
Oy 421 ASGARVYOHMRGVLLFQEPQGGHMSQVQTHGTQIGSYFGGELCGVVDVDDGETELLII 480
Db 421 ASGARVYOHMRGVLLFQEPQGGHMSQVQTHGTQIGSYFGGELCGVVDVDDGETELLII 480
Oy 481 GAPLFYGGORGRVYIYORROLGFEEVSELQDPEYPIGRFGEATLTALTDINGDLVVA 540
Db 481 GAPLFYGGORGRVYIYORROLGFEEVSELQDPEYPIGRFGEATLTALTDINGDLVVA 540
Oy 541 VGAPLEEGQAVYIFNGRHGGLSPQPSQRIEGTVLSGIQWFGRSIHGVKDLBGDLADVA 600
Db 541 VGAPLEEGQAVYIFNGRHGGLSPQPSQRIEGTVLSGIQWFGRSIHGVKDLBGDLADVA 600
Oy 601 VGASQMTVLSRPPVMDVTLMSFPAIPVHEVCSYSTSNKMEGVNITICPOIKSLI 660
Db 601 VGASQMTVLSRPPVMDVTLMSFPAIPVHEVCSYSTSNKMEGVNITICPOIKSLI 660
Oy 661 POFQGRVANTLYTLQDLGHRTRRGLPPGGRHELRRIAVTTSMSCTDFSHPVVCOD 720
Db 661 POFQGRVANTLYTLQDLGHRTRRGLPPGGRHELRRIAVTTSMSCTDFSHPVVCOD 720
Oy 721 LISPIVNSLNFSLWEEGTPRDQAGKDIPIILRSLHSETWEIPPEKNCGEDKCEAN 780
Db 721 LISPIVNSLNFSLWEEGTPRDQAGKDIPIILRSLHSETWEIPPEKNCGEDKCEAN 780

```

QY 181 DVMKLSNTSYOFAAVOFSTSYKTEPFSDYVKRKDPALLKHVKNMLLTNTTGAINVY 240  
 DB 181 DVMKLSNTSYOFAAVOFSTSYKTEPFSDYVKRKDPALLKHVKNMLLTNTTGAINVY 240  
 QY 241 ATEVEREELGARPDPATKVLIIITDGEATDSGNIDAAKOIRYIIGIGHFQTKESQETLH 300  
 DB 241 ATEVEREELGARPDPATKVLIIITDGEATDSGNIDAAKOIRYIIGIGHFQTKESQETLH 300  
 QY 301 KFAASKPASEFVKIILDTFEKLDLFTLEOKKIYVIEGTSKODLTSFNMELSSGISAADLSR 360  
 DB 301 KFAASKPASEFVKIILDTFEKLDLFTLEOKKIYVIEGTSKODLTSFNMELSSGISAADLSR 360  
 QY 361 GHAVVAVGAKDMAGGFLDLKADLDDPTFIGNEBPLTEVRAGYLGTYTWMJPSROKTSIL 420  
 DB 361 GHAVVAVGAKDMAGGFLDLKADLDDPTFIGNEBPLTEVRAGYLGTYTWMJPSROKTSIL 420  
 QY 421 ASGARPYOHMGRVLLFQEPQGGHMSOVQTIHGTOIGSYFGGELCGVDVDDGSETELLII 480  
 DB 421 ASGARPYOHMGRVLLFQEPQGGHMSOVQTIHGTOIGSYFGGELCGVDVDDGSETELLII 480  
 QY 481 GAPLFYGBORGGRVFIYORROLGFEEVSELQDPCGYLGRFGEAITALTDINGDLVDVA 540  
 DB 481 GAPLFYGBORGGRVFIYORROLGFEEVSELQDPCGYLGRFGEAITALTDINGDLVDVA 540  
 QY 541 VGAPLEBEGGAVYIENGHRGGLSPQSPORIEGTQVLSGIQWFGRSIHGYKDLBEGDLADVA 600  
 DB 541 VGAPLEBEGGAVYIENGHRGGLSPQSPORIEGTQVLSGIQWFGRSIHGYKDLBEGDLADVA 600  
 QY 601 VGASQMIIVLSSRPVDMVTLMSPSPARIPVHEVCSYSTSNKMEGVNITICFOIKSLY 660  
 DB 601 VGASQMIIVLSSRPVDMVTLMSPSPARIPVHEVCSYSTSNKMEGVNITICFOIKSLY 660  
 QY 661 POFQGRIVANLTYTLQDGHRTTRRGGLFPGGRHLEARNIAVTTSMSCDTFSHFVVCQD 720  
 DB 661 POFQGRIVANLTYTLQDGHRTTRRGGLFPGGRHLEARNIAVTTSMSCDTFSHFVVCQD 720  
 QY 721 LIJSPINVSINLSMBEGBTPRDOQAQKODIPILPISLHSETWELPFRKNCGBDKKCEAN 780  
 DB 721 LIJSPINVSINLSMBEGBTPRDOQAQKODIPILPISLHSETWELPFRKNCGBDKKCEAN 780  
 QY 781 LRVSPSPRSRLRLTAFAASLVELSLNLEBDAAVWOLDLHFRPGLSPFRKVMKXPHSO 840  
 DB 781 LRVSPSPRSRLRLTAFAASLVELSLNLEBDAAVWOLDLHFRPGLSPFRKVMKXPHSO 840  
 QY 841 IPVSCBELPEBSRLLSRALSQVSSPIFKAGSHVALQMMFNTLVNNSWGDSEYELHANTYC 900  
 DB 841 IPVSCBELPEBSRLLSRALSQVSSPIFKAGSHVALQMMFNTLVNNSWGDSEYELHANTYC 900  
 QY 901 NNBDSDLEBNSATTIIPILYIPINILIODQEDSTLYVSFTPKGPKIHQVKNMYOVIQPS 960  
 DB 901 NNBDSDLEBNSATTIIPILYIPINILIODQEDSTLYVSFTPKGPKIHQVKNMYOVIQPS 960  
 QY 961 IHDNHIPTLEAVNGVPOPPSEBPTITHQMSVQMEPPVPCHYEDLELPPAAEBCJLPGALFR 1020  
 DB 961 IHDNHIPTLEAVNGVPOPPSEBPTITHQMSVQMEPPVPCHYEDLELPPAAEBCJLPGALFR 1020  
 QY 1021 CPVYFROEILVOVIGTLEVEIEASMSFSLCSLSISFNSKHEHLVGSNLSLAQVYMK 1080  
 DB 1021 CPVYFROEILVOVIGTLEVEIEASMSFSLCSLSISFNSKHEHLVGSNLSLAQVYMK 1080  
 QY 1081 VDVIYEXKOMLYLYVLSGIGGLLLLLIFIVLYKVFPRKMLKEKMEAGRGVNGIAPADS 1140  
 DB 1081 VDVIYEXKOMLYLYVLSGIGGLLLLLIFIVLYKVFPRKMLKEKMEAGRGVNGIAPADS 1140  
 QY 1141 BOLASGOBAGDPGCKPLHEKDSSEGGKD 1170  
 DB 1141 BOLASGOBAGDPGCKPLHEKDSSEGGKD 1170

RESULT 11  
 US-09-592-617C-42  
 ; Sequence 42, Application US/09592617C

; GENERAL INFORMATION:  
 ; APPLICANT: Armout, M. Armit  
 ; TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN ANTAGONISTS  
 ; FILE REFERENCE: 00786-267002  
 ; CURRENT APPLICATION NUMBER: US/09/592,617C  
 ; PRIORITY FILING DATE: 2000-06-13  
 ; PRIOR APPLICATION NUMBER: US 08/380,167  
 ; PRIOR FILING DATE: 1999-01-30  
 ; PRIOR APPLICATION NUMBER: US 08/216,081  
 ; PRIOR FILING DATE: 1994-03-21  
 ; PRIOR APPLICATION NUMBER: US 07/637,830  
 ; PRIOR FILING DATE: 1991-01-04  
 ; PRIOR APPLICATION NUMBER: US 07/539,842  
 ; PRIOR FILING DATE: 1990-06-18  
 ; PRIOR APPLICATION NUMBER: US 07/212,573  
 ; PRIOR FILING DATE: 1988-06-28  
 ; NUMBER OF SEQ ID NOS: 72  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 42  
 ; LENGTH: 1170  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-592-617C-42

Query Match 99.9%; Score 6098; DB 19; Length 1170;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKDSCITVMAMALLSGFFFPAPASYNLDVGARSFSPRAGRHFGRVLOVNGVYIGA 60  
 DB 1 MKDSCITVMAMALLSGFFFPAPASYNLDVGARSFSPRAGRHFGRVLOVNGVYIGA 60  
 QY 61 PGBNSGSLYQCCSGTGCHCLPVLTRGSNTYSKYLGMTLADPTDGSILACDPLSRTCD 120  
 DB 61 PGBNSGSLYQCCSGTGCHCLPVLTRGSNTYSKYLGMTLADPTDGSILACDPLSRTCD 120  
 QY 121 QNTYLSGLCYLFRONLQPMLOGRPGQECIKGNVDLVFLPDGSMISQPDFQKILDFMK 180  
 DB 121 QNTYLSGLCYLFRONLQPMLOGRPGQECIKGNVDLVFLPDGSMISQPDFQKILDFMK 180  
 QY 181 DVMKLSNTSYOFAAVOFSTSYKTEPFSDYVKRKDPALLKHVKNMLLTNTTGAINVY 240  
 DB 181 DVMKLSNTSYOFAAVOFSTSYKTEPFSDYVKRKDPALLKHVKNMLLTNTTGAINVY 240  
 QY 241 ATEVEREELGARPDPATKVLIIITDGEATDSGNIDAAKOIRYIIGIGHFQTKESQETLH 300  
 DB 241 ATEVEREELGARPDPATKVLIIITDGEATDSGNIDAAKOIRYIIGIGHFQTKESQETLH 300  
 QY 301 KFAASKPASEFVKIILDTFEKLDLFTLEOKKIYVIEGTSKODLTSFNMELSSGISAADLSR 360  
 DB 301 KFAASKPASEFVKIILDTFEKLDLFTLEOKKIYVIEGTSKODLTSFNMELSSGISAADLSR 360  
 QY 361 GHAVVAVGAKDMAGGFLDLKADLDDPTFIGNEBPLTEVRAGYLGTYTWMJPSROKTSIL 420  
 DB 361 GHAVVAVGAKDMAGGFLDLKADLDDPTFIGNEBPLTEVRAGYLGTYTWMJPSROKTSIL 420  
 QY 421 ASGARPYOHMGRVLLFQEPQGGHMSOVQTIHGTOIGSYFGGELCGVDVDDGSETELLII 480  
 DB 421 ASGARPYOHMGRVLLFQEPQGGHMSOVQTIHGTOIGSYFGGELCGVDVDDGSETELLII 480  
 QY 481 GAPLFYGBORGGRVFIYORROLGFEEVSELQDPCGYLGRFGEAITALTDINGDLVDVA 540  
 DB 481 GAPLFYGBORGGRVFIYORROLGFEEVSELQDPCGYLGRFGEAITALTDINGDLVDVA 540  
 QY 541 VGAPLEBEGGAVYIENGHRGGLSPQSPORIEGTQVLSGIQWFGRSIHGYKDLBEGDLADVA 600  
 DB 541 VGAPLEBEGGAVYIENGHRGGLSPQSPORIEGTQVLSGIQWFGRSIHGYKDLBEGDLADVA 600  
 QY 601 VGASQMIIVLSSRPVDMVTLMSPSPARIPVHEVCSYSTSNKMEGVNITICFOIKSLY 660  
 DB 601 VGASQMIIVLSSRPVDMVTLMSPSPARIPVHEVCSYSTSNKMEGVNITICFOIKSLY 660  
 QY 661 POFQGRIVANLTYTLQDGHRTTRRGGLFPGGRHLEARNIAVTTSMSCDTFSHFVVCQD 720

Db 661 POFGRIVANLTYTLQLDGHRTRRGLFPGGRHELRNIAVTTSMSCDTSFHFVVCQD 720  
Qy 721 LISPIVNSLNFSLMEEBGTPRDQRAQKDIPIILRPSLSHSETWEIPEKNGCEDKCEAN 780  
Db 721 LISPIVNSLNFSLMEEBGTPRDQRAQKDIPIILRPSLSHSETWEIPEKNGCEDKCEAN 780  
Qy 781 LRVSPSPARRALRLTAFAISLVELSLNLEEDAWYQDLHPFGSLFRKVEMLKPHSQ 840  
Db 781 LRVSPSPARRALRLTAFAISLVELSLNLEEDAWYQDLHPFGSLFRKVEMLKPHSQ 840  
Qy 841 IPVCEELPEBSRLSLRSLSCNVSSPIFKAGHSVALQMMFNTLVNNSWGSDELHANTYC 900  
Db 841 IPVCEELPEBSRLSLRSLSCNVSSPIFKAGHSVALQMMFNTLVNNSWGSDELHANTYC 900  
Qy 901 NNEBSDLLEDSATTTIPIILYPINILIQDEDSITYVSFTPKGPKIHQVKMYOVRLOPS 960  
Db 901 NNEBSDLLEDSATTTIPIILYPINILIQDEDSITYVSFTPKGPKIHQVKMYOVRLOPS 960  
Qy 961 IHDNIPITLVAVGVPPSPSGPITHQMSVQMEPPVPCHEDELERLPAAEPCLPALFR 1020  
Db 961 IHDNIPITLVAVGVPPSPSGPITHQMSVQMEPPVPCHEDELERLPAAEPCLPALFR 1020  
Qy 1021 CPVVFROEILVQVIGTLELVEGEIEASSMFSLCSSLSISFNSSKPHLYGSNASLAQVVMK 1080  
Db 1021 CPVVFROEILVQVIGTLELVEGEIEASSMFSLCSSLSISFNSSKPHLYGSNASLAQVVMK 1080  
Qy 1081 VDVIYKEMKLYLVLSGIGLILLLLIIFIVLYKVGFFPKRLKEKMEAGRGVNGIPADS 1140  
Db 1081 VDVIYKEMKLYLVLSGIGLILLLLIIFIVLYKVGFFPKRLKEKMEAGRGVNGIPADS 1140  
Qy 1141 EQLASGQEAADPGCLKPLHEKDSGSGGKD 1170  
Db 1141 EQLASGQEAADPGCLKPLHEKDSGSGGKD 1170

RESULT 12  
US-09-791-537-118794  
; Sequence 118794; Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Biocomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 118794  
; LENGTH: 1170  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-791-537-118794

Query Match 99.9%; Score 6098; DB 22; Length 1170;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKDSCTIVAMALLSGFFFAPASSYNDLVGARSFPDPRAGRHEGYVLQVANGVITYGA 60  
Db 1 MKDSCTIVAMALLSGFFFAPASSYNDLVGARSFPDPRAGRHEGYVLQVANGVITYGA 60  
Qy 61 PGBENSTGSLYQCGSGTHCLPVTLRGSNTSKYLGMTLADPTDGSILACDPGLSRTCD 120  
Db 61 PGBENSTGSLYQCGSGTHCLPVTLRGSNTSKYLGMTLADPTDGSILACDPGLSRTCD 120  
Qy 121 QNTYLSGLCYLFRQMLQSPMLQGRPGFOECIKGNVDLVLFDGSMSLQPDFOKILDPMK 180  
Db 121 QNTYLSGLCYLFRQMLQSPMLQGRPGFOECIKGNVDLVLFDGSMSLQPDFOKILDPMK 180  
Qy 181 DVMKGLSNTSYQFAAVOPSTSYKTEFDSYVKRDPDALLKHVHMLLTNTFGAINVY 240

Db 181 DVMKGLSNTSYQFAAVOPSTSYKTEFDSYVKRDPDALLKHVHMLLTNTFGAINVY 240  
Qy 241 ATEVFRRELARPATVLLIITDGEATDSGNIDAAODIIRYIIGIKHQTESQETLH 300  
Db 241 ATEVFRRELARPATVLLIITDGEATDSGNIDAAODIIRYIIGIKHQTESQETLH 300  
Qy 301 KFASKPASEFVKIIDEPEKLDLFTTELQKKIYYIEGTSKODLTSFNNELSSSGISADLSR 360  
Db 301 KFASKPASEFVKIIDEPEKLDLFTTELQKKIYYIEGTSKODLTSFNNELSSSGISADLSR 360  
Qy 361 GHAVAVAGAKDWAAGFLDKADLODDTFIGNBPLTEVRAGLYGYVTWLPSPKOTSL 420  
Db 361 GHAVAVAGAKDWAAGFLDKADLODDTFIGNBPLTEVRAGLYGYVTWLPSPKOTSL 420  
Qy 421 ASGARPRQHNKRVLLPQEPQGGHMSQVOTIHGTQIGSYFGELCGVDVQDDETELLI 480  
Db 421 ASGARPRQHNKRVLLPQEPQGGHMSQVOTIHGTQIGSYFGELCGVDVQDDETELLI 480  
Qy 481 GAPLFYGEORGARVFIYQRBQLGFEEVSEIQGPBGYPFAGFGEATLALTDINGDLVDA 540  
Db 481 GAPLFYGEORGARVFIYQRBQLGFEEVSEIQGPBGYPFAGFGEATLALTDINGDLVDA 540  
Qy 541 VGAPLEBQGAVYIFNGRHGSLPQPSQRIEGTVLSGIQMPGSSIHGVKDLBGDLADVA 600  
Db 541 VGAPLEBQGAVYIFNGRHGSLPQPSQRIEGTVLSGIQMPGSSIHGVKDLBGDLADVA 600  
Qy 601 VGASQOIVLSSRVVDMTMSFPAEIPVHEGCSYISNMKEBVTITICQISLY 660  
Db 601 VGASQOIVLSSRVVDMTMSFPAEIPVHEGCSYISNMKEBVTITICQISLY 660  
Qy 661 POFGRIVANLTYTLQLDGHRTRRGLFPGGRHELRNIAVTTSMSCDTSFHFVVCQD 720  
Db 661 POFGRIVANLTYTLQLDGHRTRRGLFPGGRHELRNIAVTTSMSCDTSFHFVVCQD 720  
Qy 721 LISPIVNSLNFSLMEEBGTPRDQRAQKDIPIILRPSLSHSETWEIPEKNGCEDKCEAN 780  
Db 721 LISPIVNSLNFSLMEEBGTPRDQRAQKDIPIILRPSLSHSETWEIPEKNGCEDKCEAN 780  
Qy 781 LRVSPSPARRALRLTAFAISLVELSLNLEEDAWYQDLHPFGSLFRKVEMLKPHSQ 840  
Db 781 LRVSPSPARRALRLTAFAISLVELSLNLEEDAWYQDLHPFGSLFRKVEMLKPHSQ 840  
Qy 841 IPVCEELPEBSRLSLRSLSCNVSSPIFKAGHSVALQMMFNTLVNNSWGSDELHANTYC 900  
Db 841 IPVCEELPEBSRLSLRSLSCNVSSPIFKAGHSVALQMMFNTLVNNSWGSDELHANTYC 900  
Qy 901 NNEBSDLLEDSATTTIPIILYPINILIQDEDSITYVSFTPKGPKIHQVKMYOVRLOPS 960  
Db 901 NNEBSDLLEDSATTTIPIILYPINILIQDEDSITYVSFTPKGPKIHQVKMYOVRLOPS 960  
Qy 961 IHDNIPITLVAVGVPPSPSGPITHQMSVQMEPPVPCHEDELERLPAAEPCLPALFR 1020  
Db 961 IHDNIPITLVAVGVPPSPSGPITHQMSVQMEPPVPCHEDELERLPAAEPCLPALFR 1020  
Qy 1021 CPVVFROEILVQVIGTLELVEGEIEASSMFSLCSSLSISFNSSKPHLYGSNASLAQVVMK 1080  
Db 1021 CPVVFROEILVQVIGTLELVEGEIEASSMFSLCSSLSISFNSSKPHLYGSNASLAQVVMK 1080

RESULT 13  
US-10-170-205B-35754  
; Sequence 35754; Application US/10170205E  
; GENERAL INFORMATION:  
; APPLICANT: ADAMS, Mark

```

; TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
; TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
; FILE REFERENCE: C1001381
; CURRENT APPLICATION NUMBER: US/10/170,205E
; NUMBER OF SEQ. ID NOS: 40312
; SOFTWARE: PatentIn version 3.2
; SEQ. ID NO. 35754
; LENGTH: 1170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-170-205E-35754

```

```

Query Match      99.9%; Score 6098; DB 27; Length 1170;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKDSCITVMAMALLSGFFFPAPASSYNLDVKGARSPFPAGRHFGYRVLOVNGVYVGA 60
DB 1 MKDSCITVMAMALLSGFFFPAPASSYNLDVKGARSPFPAGRHFGYRVLOVNGVYVGA 60
QY 61 PGBNGSTGSLYQCQSGTGHCPLVTLRGSNTYSKYLGMTLATDPTDGSILACDPGLSRTCD 120
DB 61 PGBNGSTGSLYQCQSGTGHCPLVTLRGSNTYSKYLGMTLATDPTDGSILACDPGLSRTCD 120
QY 121 QNTYLSGLCYLFRONTLQGPMLQGRPGFOECIKGNVDVFLPFGSGMSLQPDFOKILDFMK 180
DB 121 QNTYLSGLCYLFRONTLQGPMLQGRPGFOECIKGNVDVFLPFGSGMSLQPDFOKILDFMK 180
QY 181 DVNKLSTSYQFAVQSTSYKTEPDSVDYKRDPAALKHVGMILLNTTGAINYV 240
DB 181 DVNKLSTSYQFAVQSTSYKTEPDSVDYKRDPAALKHVGMILLNTTGAINYV 240
QY 241 ATBVRREELGARPDATKVLIIITDGEATDSGNIDAADIIIRYIIGIGHFOTKESQETLH 300
DB 241 ATBVRREELGARPDATKVLIIITDGEATDSGNIDAADIIIRYIIGIGHFOTKESQETLH 300
QY 301 KFAKSPASEFVKILDFTEKLKDLFTELQKKIYVIEGTSKODLTSFNMELSSSGISADLSR 360
DB 301 KFAKSPASEFVKILDFTEKLKDLFTELQKKIYVIEGTSKODLTSFNMELSSSGISADLSR 360
QY 361 GHAVVGAAGAKDAGGLDLKADLDDPTFIGNBFLPEVRAGYLYVTWMLPSROKSTSL 420
DB 361 GHAVVGAAGAKDAGGLDLKADLDDPTFIGNBFLPEVRAGYLYVTWMLPSROKSTSL 420
QY 421 ASDAPRYQMGGRVLLFOEPQGGGSHWSQYQTIHGTOIGSYFGGELCGVVDVDDGETELLII 480
DB 421 ASDAPRYQMGGRVLLFOEPQGGGSHWSQYQTIHGTOIGSYFGGELCGVVDVDDGETELLII 480
QY 481 GAPLFYQGRQGRVFTYQRRQLGFEVESELQGDPEYPLGRFGEAITLALTDINGDLVDVA 540
DB 481 GAPLFYQGRQGRVFTYQRRQLGFEVESELQGDPEYPLGRFGEAITLALTDINGDLVDVA 540
QY 541 VGAPLEEGGAYYIFNGRHGGLSPQSPQRIEGTQVLSGIQWFGRSIHGVKDLBGDLAAYA 600
DB 541 VGAPLEEGGAYYIFNGRHGGLSPQSPQRIEGTQVLSGIQWFGRSIHGVKDLBGDLAAYA 600
QY 601 VGASQOMTVLSRPVVDVTLMSFSPARIPVHEVCSYSTSNKMEGNVITICFOIKSLY 660
DB 601 VGASQOMTVLSRPVVDVTLMSFSPARIPVHEVCSYSTSNKMEGNVITICFOIKSLY 660
QY 661 POFQGRVLAANTYTLQLDGHTRRRGLPFGGHEILRNIAVTTSMSCDTSFHFPPVQVD 720
DB 661 POFQGRVLAANTYTLQLDGHTRRRGLPFGGHEILRNIAVTTSMSCDTSFHFPPVQVD 720
QY 721 LIISPINVLNFSIMEEGTPRDQAGKDIPILRPSLSHETWELPERKNGEDKKCAN 780
DB 721 LIISPINVLNFSIMEEGTPRDQAGKDIPILRPSLSHETWELPERKNGEDKKCAN 780
QY 781 LRVSPSPASRALRLTAFAASLVELSLANLEEDATWVOLDLHFPGLSFRKVEMLKPHSQ 840
DB 781 LRVSPSPASRALRLTAFAASLVELSLANLEEDATWVOLDLHFPGLSFRKVEMLKPHSQ 840

```

```

QY 841 IPVSCBELPERSRLLSRASCNVSPITFKASHVALQMMFNTLVNNSGKDSVELHANATC 900
DB 841 IPVSCBELPERSRLLSRASCNVSPITFKASHVALQMMFNTLVNNSGKDSVELHANATC 900
QY 901 NNEBSDLLEDSNATTTIPIILPINILIQDQDSTLYVSPFKGPKIHQVKMYQVRLOPS 960
DB 901 NNEBSDLLEDSNATTTIPIILPINILIQDQDSTLYVSPFKGPKIHQVKMYQVRLOPS 960
QY 961 IHDNIPITLNAVGVPOPPSEGPITTHQMSVQMEPPVPCHEDELRLLPDAAPCLPGLALFR 1020
DB 961 IHDNIPITLNAVGVPOPPSEGPITTHQMSVQMEPPVPCHEDELRLLPDAAPCLPGLALFR 1020
QY 1021 CPVVRQETILVQVIGTLELVEIEASQWFSICSSLSISFNSKPHLYGSNASIAQVVMK 1080
DB 1021 CPVVRQETILVQVIGTLELVEIEASQWFSICSSLSISFNSKPHLYGSNASIAQVVMK 1080
QY 1081 DVVYERQMLYLYLSGIGILLDLILFIVLYKYGFKPRNLEKMEAGRGVPGNIPAEBS 1140
DB 1081 DVVYERQMLYLYLSGIGILLDLILFIVLYKYGFKPRNLEKMEAGRGVPGNIPAEBS 1140
QY 1141 EQLASQDAGDPGLKPLHEKDSGSGGKD 1170
DB 1141 EQLASQDAGDPGLKPLHEKDSGSGGKD 1170

RESULT 14
US-10-261-164-1
; Sequence 1, Application US/10261164
; GENERAL INFORMATION:
; APPLICANT: KAPUSTAV, PAMELA M.
; TITLE OF INVENTION: LFA-1 ALPHA SUBUNIT ANTIBODIES AND METHODS OF USE
; FILE REFERENCE: 046007/0272304
; CURRENT APPLICATION NUMBER: US/10/261,164
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ. ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ. ID NO. 1
; LENGTH: 1170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-261-164-1

Query Match      99.9%; Score 6098; DB 28; Length 1170;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKDSCITVMAMALLSGFFFPAPASSYNLDVKGARSPFPAGRHFGYRVLOVNGVYVGA 60
DB 1 MKDSCITVMAMALLSGFFFPAPASSYNLDVKGARSPFPAGRHFGYRVLOVNGVYVGA 60
QY 61 PGBNGSTGSLYQCQSGTGHCPLVTLRGSNTYSKYLGMTLATDPTDGSILACDPGLSRTCD 120
DB 61 PGBNGSTGSLYQCQSGTGHCPLVTLRGSNTYSKYLGMTLATDPTDGSILACDPGLSRTCD 120
QY 121 QNTYLSGLCYLFRONTLQGPMLQGRPGFOECIKGNVDVFLPFGSGMSLQPDFOKILDFMK 180
DB 121 QNTYLSGLCYLFRONTLQGPMLQGRPGFOECIKGNVDVFLPFGSGMSLQPDFOKILDFMK 180
QY 181 DVNKLSTSYQFAVQSTSYKTEPDSVDYKRDPAALKHVGMILLNTTGAINYV 240
DB 181 DVNKLSTSYQFAVQSTSYKTEPDSVDYKRDPAALKHVGMILLNTTGAINYV 240
QY 241 ATBVRREELGARPDATKVLIIITDGEATDSGNIDAADIIIRYIIGIGHFOTKESQETLH 300
DB 241 ATBVRREELGARPDATKVLIIITDGEATDSGNIDAADIIIRYIIGIGHFOTKESQETLH 300
QY 301 KFAKSPASEFVKILDFTEKLKDLFTELQKKIYVIEGTSKODLTSFNMELSSSGISADLSR 360
DB 301 KFAKSPASEFVKILDFTEKLKDLFTELQKKIYVIEGTSKODLTSFNMELSSSGISADLSR 360
QY 361 GHAVVGAAGAKDAGGLDLKADLDDPTFIGNBFLPEVRAGYLYVTWMLPSROKSTSL 420
DB 361 GHAVVGAAGAKDAGGLDLKADLDDPTFIGNBFLPEVRAGYLYVTWMLPSROKSTSL 420

```

Db 361 GHAUVAGAKDMAGFLDLKADLDDTFIGNBPLTEPRVAGYLGVTWLPSPROKTSLL 420  
Qy 421 ASGAPRYOHMGRVLLFQEPQGGHWSQVQTIHGTOIGSYFGGELCGVDDODGETELLII 480  
Db 421 ASGAPRYOHMGRVLLFQEPQGGHWSQVQTIHGTOIGSYFGGELCGVDDODGETELLII 480  
Qy 481 GAPLFYGEORGRVFIYQRRQLGFEVESELQDPGYPGRRGAIATLTDINDGLVDVA 540  
Db 481 GAPLFYGEORGRVFIYQRRQLGFEVESELQDPGYPGRRGAIATLTDINDGLVDVA 540  
Qy 541 VGAPLEEGGAVYIFNGRHGGLSPQPSQRIEGTOVLSGIQMGFRSHIGYKDLLEGGLADVA 600  
Db 541 VGAPLEEGGAVYIFNGRHGGLSPQPSQRIEGTOVLSGIQMGFRSHIGYKDLLEGGLADVA 600  
Qy 601 VGASQMTVLSSRPVDDMTLMSFPAIPVHEVCSYSTSNKMKEGVNTTCFOIKSLY 660  
Db 601 VGASQMTVLSSRPVDDMTLMSFPAIPVHEVCSYSTSNKMKEGVNTTCFOIKSLY 660  
Qy 661 POFQGRLVANLTYTLQDGHRTTRRGLPFGGRHBLRNIAVTTSMSCDPSFHPVVCVD 720  
Db 661 POFQGRLVANLTYTLQDGHRTTRRGLPFGGRHBLRNIAVTTSMSCDPSFHPVVCVD 720  
Qy 721 LISPIVNSLNFSLMBEETPRDQRAQKDIPIILRPSLHSETWEIPFKXNGEDKCEAN 780  
Db 721 LISPIVNSLNFSLMBEETPRDQRAQKDIPIILRPSLHSETWEIPFKXNGEDKCEAN 780  
Qy 781 LRVFSFSPARSRALRLTAPASLSVELSLNLEDAVWVOLDLHPPGSLFRKVMKPHSQ 840  
Db 781 LRVFSFSPARSRALRLTAPASLSVELSLNLEDAVWVOLDLHPPGSLFRKVMKPHSQ 840  
Qy 841 IPVSCBELPESRLLSRALSQNVSSPIFKAGHVALQMMFNTLVNSWGDSEVELHANVTC 900  
Db 841 IPVSCBELPESRLLSRALSQNVSSPIFKAGHVALQMMFNTLVNSWGDSEVELHANVTC 900  
Qy 901 NNEBSDLLEDSATTIIPILYPIINLIDODDSTLYSFTPKGPRKHQVKNMYOVRLOPS 960  
Db 901 NNEBSDLLEDSATTIIPILYPIINLIDODDSTLYSFTPKGPRKHQVKNMYOVRLOPS 960  
Qy 961 IHDNRIPTLBAVGVPOPPSEGPITHQMSVOMEPVPCHYEDLELPPAAEPCLPGALFR 1020  
Db 961 IHDNRIPTLBAVGVPOPPSEGPITHQMSVOMEPVPCHYEDLELPPAAEPCLPGALFR 1020  
Qy 1021 CPVFEROELIYOVIETLEVEIEASMSFSLCSLSISFNSSKHHLVGSNLSLAQVVMK 1080  
Db 1021 CPVFEROELIYOVIETLEVEIEASMSFSLCSLSISFNSSKHHLVGSNLSLAQVVMK 1080  
Qy 1081 VDVFYKMKMLTYLVSIGIGILLLLIPIYVYKGFPPKRNKEKMEAGRGVPPNGI PAEDS 1140  
Db 1081 VDVFYKMKMLTYLVSIGIGILLLLIPIYVYKGFPPKRNKEKMEAGRGVPPNGI PAEDS 1140  
Qy 1141 EQLASGOEADPGCLPKLHEKDSGGGKD 1170  
Db 1141 EQLASGOEADPGCLPKLHEKDSGGGKD 1170

## RESULT 15

us-10-325-899-9350  
; Sequence 9350, Application US/10325899  
; GENERAL INFORMATION:  
; APPLICANT: Wohlgenuth, Jay  
; APPLICANT: Fry, Kirk  
; APPLICANT: Ly, Ngoc  
; APPLICANT: Woodward, Robert  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING TRANSPLANT  
; TITLE OF INVENTION: REJECTION  
; FILE REFERENCE: 506612000122  
; CURRENT APPLICATION NUMBER: US/10/325, 899  
; PRIOR FILING DATE: 2002-12-20  
; PRIOR APPLICATION NUMBER: US 60/296, 764  
; PRIOR FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 10/006, 290  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: US 10/131, 831

; PRIOR FILING DATE: 2002-04-24  
; NUMBER OF SEQ ID NOS: 996  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9350  
; LENGTH: 1170  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
us-10-325-899-9350

Query Match 99.9%; Score 6098; DB 29; Length 1170;

Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKDSCTVMAMALLSGFFFPAPASVYLDVDRGARSFPFPAGRHFGYVLOVNGVYVGA 60  
Db 1 MKDSCTVMAMALLSGFFFPAPASVYLDVDRGARSFPFPAGRHFGYVLOVNGVYVGA 60  
Qy 61 PEGNSTGSLYQCSGTGHCPLVTLRGSNTSKYLQMTLATDPTDGSIIACDPGLSRTCD 120  
Db 61 PEGNSTGSLYQCSGTGHCPLVTLRGSNTSKYLQMTLATDPTDGSIIACDPGLSRTCD 120  
Qy 121 QNTYLSGLCYLFRQNLQGPMLQGRPGFQECIKANVDLVEFLPDSMSIQDPFQKIIDFMK 180  
Db 121 QNTYLSGLCYLFRQNLQGPMLQGRPGFQECIKANVDLVEFLPDSMSIQDPFQKIIDFMK 180  
Qy 181 DVMKLSNTSYQPAVQFSTSYKTEPFDSDYVRKDPDALLKHKVHMLLTNTFGAIVNV 240  
Db 181 DVMKLSNTSYQPAVQFSTSYKTEPFDSDYVRKDPDALLKHKVHMLLTNTFGAIVNV 240  
Qy 241 ATEVFREELGAPDPAATVLLIITDGEATDSGNIDAANDIIRYIIIGIKHFQYKESQETLH 300  
Db 241 ATEVFREELGAPDPAATVLLIITDGEATDSGNIDAANDIIRYIIIGIKHFQYKESQETLH 300  
Qy 301 KPAKSPASEFVKIIDPEKIKDLFTBLQKKIYVIEGSKODLTSFNNESSSGISADLSR 360  
Db 301 KPAKSPASEFVKIIDPEKIKDLFTBLQKKIYVIEGSKODLTSFNNESSSGISADLSR 360  
Qy 361 GHAUVAGAKDMAGFLDLKADLDDTFIGNBPLTEPRVAGYLGVTWLPSPROKTSLL 420  
Db 361 GHAUVAGAKDMAGFLDLKADLDDTFIGNBPLTEPRVAGYLGVTWLPSPROKTSLL 420  
Qy 421 ASGAPRYOHMGRVLLFQEPQGGHWSQVQTIHGTOIGSYFGGELCGVDDODGETELLII 480  
Db 421 ASGAPRYOHMGRVLLFQEPQGGHWSQVQTIHGTOIGSYFGGELCGVDDODGETELLII 480  
Qy 481 GAPLFYGEORGRVFIYQRRQLGFEVESELQDPGYPGRRGAIATLTDINDGLVDVA 540  
Db 481 GAPLFYGEORGRVFIYQRRQLGFEVESELQDPGYPGRRGAIATLTDINDGLVDVA 540  
Qy 541 VGAPLEEGGAVYIFNGRHGGLSPQPSQRIEGTOVLSGIQMGFRSHIGYKDLLEGGLADVA 600  
Db 541 VGAPLEEGGAVYIFNGRHGGLSPQPSQRIEGTOVLSGIQMGFRSHIGYKDLLEGGLADVA 600  
Qy 601 VGASQMTVLSSRPVDDMTLMSFPAIPVHEVCSYSTSNKMKEGVNTTCFOIKSLY 660  
Db 601 VGASQMTVLSSRPVDDMTLMSFPAIPVHEVCSYSTSNKMKEGVNTTCFOIKSLY 660  
Qy 661 POFQGRLVANLTYTLQDGHRTTRRGLPFGGRHBLRNIAVTTSMSCDPSFHPVVCVD 720  
Db 661 POFQGRLVANLTYTLQDGHRTTRRGLPFGGRHBLRNIAVTTSMSCDPSFHPVVCVD 720  
Qy 721 LISPIVNSLNFSLMBEETPRDQRAQKDIPIILRPSLHSETWEIPFKXNGEDKCEAN 780  
Db 721 LISPIVNSLNFSLMBEETPRDQRAQKDIPIILRPSLHSETWEIPFKXNGEDKCEAN 780  
Qy 781 LRVFSFSPARSRALRLTAPASLSVELSLNLEDAVWVOLDLHPPGSLFRKVMKPHSQ 840  
Db 781 LRVFSFSPARSRALRLTAPASLSVELSLNLEDAVWVOLDLHPPGSLFRKVMKPHSQ 840  
Qy 841 IPVSCBELPESRLLSRALSQNVSSPIFKAGHVALQMMFNTLVNSWGDSEVELHANVTC 900  
Db 841 IPVSCBELPESRLLSRALSQNVSSPIFKAGHVALQMMFNTLVNSWGDSEVELHANVTC 900

Qy	901	NNEDSDLEEDNSATTIIPILYPINILIOEDSTLYVSFTPKGIHQKMYQVRIQPS	960
Db	901	NNEDSDLEEDNSATTIIPILYPINILIOEDSTLYVSFTPKGIHQKMYQVRIQPS	960
Qy	961	IHDHNIPTLEAVGVGPSPSEGPITHQMSVQMEPPVPCHYEDLERLPDAEPCLEPGLFR	1020
Db	961	IHDHNIPTLEAVGVGPSPSEGPITHQMSVQMEPPVPCHYEDLERLPDAEPCLEPGLFR	1020
Qy	1021	CPVVRROELIVQVIGTLELVGEIEASSMPSLCSSTISFNSKPHLYGNSASLAQVVMK	1080
Db	1021	CPVVRROELIVQVIGTLELVGEIEASSMPSLCSSTISFNSKPHLYGNSASLAQVVMK	1080
Qy	1081	VDVVEKQMLYLYVLSGIGLLILLIFLYLYKVGFPRKRLKEKMEAGRGVNGIPEADS	1140
Db	1081	VDVVEKQMLYLYVLSGIGLLILLIFLYLYKVGFPRKRLKEKMEAGRGVNGIPEADS	1140
Qy	1141	EQLASGQEAQDPCGCKPLHEKDSSESGGKD	1170
Db	1141	EQLASGQEAQDPCGCKPLHEKDSSESGGKD	1170

Search completed: August 29, 2005, 19:35:37  
 Job time : 489 secs



This Page Blank (uspto)

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: August 29, 2005, 19:21:54 ; Search time 86 Seconds  
(without alignments)  
2139.235 Million cell updates/sec

Title: US-09-945-265-2

Perfect score: 6106  
Sequence: 1 MKDSCITVMAMALLSGFFFF.....DPGLKPLKEDSRSGGKGD 1170

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 729853 seqs, 15724287 residues

Total number of hits satisfying chosen parameters: 729853

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents AA New:\*  
1: /cgn2\_6/ptodata/2/paa/PCT\_NEW\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/paa/US06\_NEW\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/paa/US07\_NEW\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/paa/US08\_NEW\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/paa/US10\_NEW\_COMB.pep:\*  
7: /cgn2\_6/ptodata/2/paa/US11\_NEW\_COMB.pep:\*  
8: /cgn2\_6/ptodata/2/paa/US60\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6106	100.0	1170	1 PCT-US05-02350-142	Sequence 142, App
2	6106	100.0	1170	7 US-11-043-770-142	Sequence 142, App
3	6106	100.0	1170	7 US-11-080-026-2	Sequence 2, Appli
4	6106	100.0	1170	7 US-11-107-028-4	Sequence 2, Appli
5	6098	99.9	1170	1 PCT-US05-02350-653	Sequence 653, App
6	6098	99.9	1170	5 US-09-976-935A-36	Sequence 36, Appli
7	6098	99.9	1170	7 US-11-043-770-653	Sequence 653, App
8	6098	99.9	1170	7 US-11-062-290-1	Sequence 1, Appli
9	6053.5	99.1	1223	1 PCT-US03-10870-295	Sequence 295, App
10	5981	98.0	1145	7 US-11-021-951-130	Sequence 130, App
11	5585	91.5	1086	1 PCT-US03-10870-1871	Sequence 1871, App
12	3885	63.6	750	1 PCT-US05-02350-80	Sequence 80, Appli
13	3885	63.6	750	7 US-11-043-770-80	Sequence 80, Appli
14	3066	50.2	589	7 US-11-062-290-2	Sequence 2, Appli
15	1564	25.6	1154	8 US-60-651-235-76	Sequence 76, Appli
16	1564	25.6	1154	8 US-60-680-004-144	Sequence 144, App
17	1564	25.6	1154	8 US-60-701-054-258	Sequence 258, App
18	1563.5	25.6	1152	8 US-60-651-235-74	Sequence 74, Appli
19	1563.5	25.6	1152	8 US-60-651-235-77	Sequence 77, Appli
20	1563.5	25.6	1153	8 US-60-680-004-145	Sequence 145, App
21	1563.5	25.6	1153	8 US-60-701-054-259	Sequence 259, App
22	1562.5	25.6	1152	1 PCT-US05-02350-141	Sequence 141, App
23	1562.5	25.6	1152	7 US-11-043-770-141	Sequence 141, App
24	1562.5	25.6	1152	7 US-11-080-026-4	Sequence 4, Appli
25	1562.5	25.6	1152	8 US-60-651-235-75	Sequence 75, Appli

26	1562.5	25.6	1152	8 US-60-680-004-143	Sequence 143, App
27	1562.5	25.6	1152	8 US-60-701-054-257	Sequence 257, App
28	1154.5	18.9	1217	6 US-10-940-774A-7892	Sequence 7892, App
29	1154	18.9	1189	6 US-10-450-763-43308	Sequence 43308, A
30	1149.5	18.8	1188	7 US-11-175-714-147	Sequence 147, App
31	1146.5	18.8	1188	5 US-09-960-403A-2	Sequence 2, Appli
32	1139	18.7	1166	7 US-11-175-714-148	Sequence 148, App
33	1132	18.4	1188	7 US-11-175-714-165	Sequence 165, App
34	1121.5	18.4	1177	8 US-60-664-611-976	Sequence 976, App
35	1121.5	18.4	1177	8 US-60-664-936-459	Sequence 459, App
36	1121.5	18.4	1178	7 US-11-154-939-951	Sequence 951, App
37	1121.5	18.4	1178	7 US-11-167-575-951	Sequence 951, App
38	1121.5	18.4	1178	8 US-60-679-970-847	Sequence 847, App
39	1121.5	18.4	1178	8 US-60-680-002-508	Sequence 508, App
40	1117.5	18.3	1179	7 US-11-154-939-950	Sequence 950, App
41	1117.5	18.3	1179	7 US-11-167-575-950	Sequence 950, App
42	1117.5	18.3	1179	8 US-60-664-611-975	Sequence 975, App
43	1117.5	18.3	1179	8 US-60-664-936-458	Sequence 458, App
44	1117.5	18.3	1179	8 US-60-679-970-843	Sequence 843, App
45	1117.5	18.3	1179	8 US-60-680-002-504	Sequence 504, App

ALIGNMENTS

RESULT 1  
PCT-US05-02350-142  
Sequence 142, Application PC/TUS0502350  
GENERAL INFORMATION:  
APPLICANT: Ayalon-Soffer, Michal  
APPLICANT: Levine, Zurit  
APPLICANT: Sella-Tavor, Osnat  
APPLICANT: Diber, Alex  
APPLICANT: Shemesh, Ronen  
APPLICANT: Toporik, Amir  
APPLICANT: Rotman, Galit  
APPLICANT: Nemzer, Sergey  
APPLICANT: Rosenberg, Avi  
APPLICANT: Dahan, Dvir  
APPLICANT: Wool, Assaf  
APPLICANT: Kojocanu, Gad S.  
APPLICANT: Aktva, Plinchas  
APPLICANT: Pollock, Sarah  
APPLICANT: Savitsky, Kineret  
APPLICANT: Bernstein, Jeanne  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES ENCODING POLYPEPTIDES AND METHODS USING  
FILE REFERENCE: 28487  
CURRENT APPLICATION NUMBER: PCT/US05/02350  
CURRENT FILING DATE: 2005-02-10  
NUMBER OF SEQ ID NOS: 1155  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 142  
LENGTH: 1170  
TYPE: PRT  
ORGANISM: Homo sapiens  
PCT-US05-02350-142  
Query Match 100.0%; Score 6106; DB 1; Length 1170;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKDSCITVMAMALLSGFFFPASSYMLDVGARSFSPRAGRHFGRVLOVNGVYGA 60  
DB 1 MKDSCITVMAMALLSGFFFPASSYMLDVGARSFSPRAGRHFGRVLOVNGVYGA 60  
QY 61 PGEAGNSGSLYQCCSGGHCIPVTLRGSNTSKYLTGTLATDPTDGSILACDPLSTRCD 120  
DB 61 PGEAGNSGSLYQCCSGGHCIPVTLRGSNTSKYLTGTLATDPTDGSILACDPLSTRCD 120  
QY 121 QNTYLSGICVYLFRONLQGPMLQGRPGFOECIKGNVDLVFLPDGSMISLOPDEFQKILDFPMK 180  
DB 121 QNTYLSGICVYLFRONLQGPMLQGRPGFOECIKGNVDLVFLPDGSMISLOPDEFQKILDFPMK 180

QY 181 DVMKLSNTSYQFAVQFSTSYKTEPDSYVYKRDPAALAKHVAKMLLNTFGAINVY 240  
DB 181 DVMKLSNTSYQFAVQFSTSYKTEPDSYVYKRDPAALAKHVAKMLLNTFGAINVY 240  
QY 241 ATEVFRBELGARPDATKVLIIITDGEATDSGNIDAADKIIRYIIIGIKHPQTKESQETLH 300  
DB 241 ATEVFRBELGARPDATKVLIIITDGEATDSGNIDAADKIIRYIIIGIKHPQTKESQETLH 300  
QY 301 KFAKSPASEFVKIIDTEPEKLDLFTLEOKKIYVIEGTSKODLTSFNMELSSSGISADLSR 360  
DB 301 KFAKSPASEFVKIIDTEPEKLDLFTLEOKKIYVIEGTSKODLTSFNMELSSSGISADLSR 360  
QY 361 GHAVVAVGAKDMAGGFLDLKADLQDDFTFIGNBPLTEPVRAGYLYVTWMLPSRQKTSLL 420  
DB 361 GHAVVAVGAKDMAGGFLDLKADLQDDFTFIGNBPLTEPVRAGYLYVTWMLPSRQKTSLL 420  
QY 421 ASGAPRYQHMGRVLLFQEPQGGGHSQVQTIHGTOIGSYFGGELCGVDVDDGTELLLI 480  
DB 421 ASGAPRYQHMGRVLLFQEPQGGGHSQVQTIHGTOIGSYFGGELCGVDVDDGTELLLI 480  
QY 481 GAPLFYGEORGRVFIYORROLGFEVESELQDPCGYLGRGEGATLTALDINGGLADVA 540  
DB 481 GAPLFYGEORGRVFIYORROLGFEVESELQDPCGYLGRGEGATLTALDINGGLADVA 540  
QY 541 VGAPLEBQGAUYIIFNGRHGGLSPQSPQRIEGTOVLSGIQWFGRSIHGVKDEGDLADVA 600  
DB 541 VGAPLEBQGAUYIIFNGRHGGLSPQSPQRIEGTOVLSGIQWFGRSIHGVKDEGDLADVA 600  
QY 601 VGASQOMTVLSSRPVDMVTLMSPBAIPVHEVCSTYSNKMKEGVNITTCQIKSLY 660  
DB 601 VGASQOMTVLSSRPVDMVTLMSPBAIPVHEVCSTYSNKMKEGVNITTCQIKSLY 660  
QY 661 POFQGRVANTLTTLTOLDGHRTRRGLPFGGRHELRNIAATTSMSCTDPSFHPVQCQD 720  
DB 661 POFQGRVANTLTTLTOLDGHRTRRGLPFGGRHELRNIAATTSMSCTDPSFHPVQCQD 720  
QY 721 LISPINVSLNFSLEEBEGTPRDORAQKODIPILRLPSLHSETWEIPEFKNCGEDKCBAN 780  
DB 721 LISPINVSLNFSLEEBEGTPRDORAQKODIPILRLPSLHSETWEIPEFKNCGEDKCBAN 780  
QY 781 LRVSPSPARSAKLTLTAPASLSVEISLNLBEDAVVOLDLHPPGLSFRKVEMLKPHSQ 840  
DB 781 LRVSPSPARSAKLTLTAPASLSVEISLNLBEDAVVOLDLHPPGLSFRKVEMLKPHSQ 840  
QY 841 IPVSCBELPEERSRLSLRASCNVSSPIFKAGHSVALQWMPNTLVNSSWGDVVELHANVTC 900  
DB 841 IPVSCBELPEERSRLSLRASCNVSSPIFKAGHSVALQWMPNTLVNSSWGDVVELHANVTC 900  
QY 901 NNEBSDDLSDNSATTTIPIILYPINILIQDQDSTLYSFTPKGPKIHQVKMAYQVRIQPS 960  
DB 901 NNEBSDDLSDNSATTTIPIILYPINILIQDQDSTLYSFTPKGPKIHQVKMAYQVRIQPS 960  
QY 961 IHDNRPITLNAVGVPOPSPSEGPITTHQMSVQMEPPVPCHEYDLERLPDAAPCLPGALFR 1020  
DB 961 IHDNRPITLNAVGVPOPSPSEGPITTHQMSVQMEPPVPCHEYDLERLPDAAPCLPGALFR 1020  
QY 1021 CPVVPQOIIIVOVIGTELVEIEIASSMFSLCSSLISIFNSSKPHLYGSMASLAQVVMK 1080  
DB 1021 CPVVPQOIIIVOVIGTELVEIEIASSMFSLCSSLISIFNSSKPHLYGSMASLAQVVMK 1080  
QY 1081 VDVIYVEKQMLLYLVLSGIGILLLLLLIIVLYKVVFPGKRLKEKMEAGRGVPMGIPADS 1140  
DB 1081 VDVIYVEKQMLLYLVLSGIGILLLLLLIIVLYKVVFPGKRLKEKMEAGRGVPMGIPADS 1140  
QY 1141 EQLASQGEAGDPGCLKPLHERKDSBGSGKD 1170  
DB 1141 EQLASQGEAGDPGCLKPLHERKDSBGSGKD 1170

RESULT 2

US-11-043-770-142

; Sequence 142; Application US/11043770

GENERAL INFORMATION:  
APPLICANT: Ayalon-Soffer, Michael  
APPLICANT: Levine, Zurit  
APPLICANT: Sella-Tavor, Osnat  
APPLICANT: Diber, Alex  
APPLICANT: Shemesh, Ronen  
APPLICANT: Toporik, Amir  
APPLICANT: Rotman, Galit  
APPLICANT: Nemzer, Sergey  
APPLICANT: Rosenberg, Avi  
APPLICANT: Danary, Dvir  
APPLICANT: Wool, Assaf  
APPLICANT: Cojocaru, Gad S.  
APPLICANT: Akiva, Pinchas  
APPLICANT: Pollock, Sarah  
APPLICANT: Savitsky, Kimeret  
APPLICANT: Bernstein, Jeanne  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES ENCODING POLYPEPTIDES AND METHODS USING  
FILE REFERENCE: 28488  
CURRENT APPLICATION NUMBER: US/11/043, 770  
NUMBER OF SEQ ID NOS: 1155  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 142  
LENGTH: 1170  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-043-770-142

Query Match 100.0%; Score 6106; DB 7; Length 1170;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKDSCTVMAALLSGFFPAPASNYLDVRGARSFSPAPAGRHGRVYQVNGVYVGA 60  
DB 1 MKDSCTVMAALLSGFFPAPASNYLDVRGARSFSPAPAGRHGRVYQVNGVYVGA 60  
QY 61 PGBNSTGSLYOCOSGCHCLPVTLRGSNTSKYLGMTLATDPPDGSILACDPGLSRTCD 120  
DB 61 PGBNSTGSLYOCOSGCHCLPVTLRGSNTSKYLGMTLATDPPDGSILACDPGLSRTCD 120  
QY 121 QNTYLSGLCYLFRONTQGPMLQGRPGFOECIKGNVDLVFLFDGSMSLQDPFOKILDFMK 180  
DB 121 QNTYLSGLCYLFRONTQGPMLQGRPGFOECIKGNVDLVFLFDGSMSLQDPFOKILDFMK 180  
QY 181 DVMKLSNTSYQFAVQFSTSYKTEPDSYVYKRDPAALAKHVAKMLLNTFGAINVY 240  
DB 181 DVMKLSNTSYQFAVQFSTSYKTEPDSYVYKRDPAALAKHVAKMLLNTFGAINVY 240  
QY 241 ATEVFRBELGARPDATKVLIIITDGEATDSGNIDAADKIIRYIIIGIKHPQTKESQETLH 300  
DB 241 ATEVFRBELGARPDATKVLIIITDGEATDSGNIDAADKIIRYIIIGIKHPQTKESQETLH 300  
QY 301 KFAKSPASEFVKIIDTEPEKLDLFTLEOKKIYVIEGTSKODLTSFNMELSSSGISADLSR 360  
DB 301 KFAKSPASEFVKIIDTEPEKLDLFTLEOKKIYVIEGTSKODLTSFNMELSSSGISADLSR 360  
QY 361 GHAVVAVGAKDMAGGFLDLKADLQDDFTFIGNBPLTEPVRAGYLYVTWMLPSRQKTSLL 420  
DB 361 GHAVVAVGAKDMAGGFLDLKADLQDDFTFIGNBPLTEPVRAGYLYVTWMLPSRQKTSLL 420  
QY 421 ASGAPRYQHMGRVLLFQEPQGGGHSQVQTIHGTOIGSYFGGELCGVDVDDGTELLLI 480  
DB 421 ASGAPRYQHMGRVLLFQEPQGGGHSQVQTIHGTOIGSYFGGELCGVDVDDGTELLLI 480  
QY 481 GAPLFYGEORGRVFIYORROLGFEVESELQDPCGYLGRGEGATLTALDINGGLADVA 540  
DB 481 GAPLFYGEORGRVFIYORROLGFEVESELQDPCGYLGRGEGATLTALDINGGLADVA 540  
QY 541 VGAPLEBQGAUYIIFNGRHGGLSPQSPQRIEGTOVLSGIQWFGRSIHGVKDEGDLADVA 600  
DB 541 VGAPLEBQGAUYIIFNGRHGGLSPQSPQRIEGTOVLSGIQWFGRSIHGVKDEGDLADVA 600

QY 601 VQAESOMIVLSRPPVDMVTLMSPSPAPIPVHEVCSTYSNKMKEGVNITTCFOIKSLY 660  
DB 601 VQAESOMIVLSRPPVDMVTLMSPSPAPIPVHEVCSTYSNKMKEGVNITTCFOIKSLY 660  
QY 661 POFQGRUVANLTYTLODGHRTTRRGLPFGGRHRLRNIAVTTSMSCDTSFHFVPCVD 720  
DB 661 POFQGRUVANLTYTLODGHRTTRRGLPFGGRHRLRNIAVTTSMSCDTSFHFVPCVD 720  
QY 721 LISPINVSLNFSLWEEBGTPRDQRAQKDIPIILRPSLSHSETWEIPEKNCGEKCCGAN 780  
DB 721 LISPINVSLNFSLWEEBGTPRDQRAQKDIPIILRPSLSHSETWEIPEKNCGEKCCGAN 780  
QY 781 LRVSPSPARSRLRLTAAPASLSVELSLNLEBDAYVQDLHFPFGLSFRKVENLKPBSQ 840  
DB 781 LRVSPSPARSRLRLTAAPASLSVELSLNLEBDAYVQDLHFPFGLSFRKVENLKPBSQ 840  
QY 841 IPVSCBELPEBSRLSRALSCNVSSPIFKAGHSVALQMMFNTLVNSWGDSEVELHANVTC 900  
DB 841 IPVSCBELPEBSRLSRALSCNVSSPIFKAGHSVALQMMFNTLVNSWGDSEVELHANVTC 900  
QY 901 NNBSDDLLEDSNATITIPILYPINILIDQEDSTLYVSFTPKGPKIHQKMYQVRIQPS 960  
DB 901 NNBSDDLLEDSNATITIPILYPINILIDQEDSTLYVSFTPKGPKIHQKMYQVRIQPS 960  
QY 961 IHDNIPITLEAVGVPOPPSEGPITHQWSVQMEPPVPCHEYDELRPLDAEPCLPGLAFR 1020  
DB 961 IHDNIPITLEAVGVPOPPSEGPITHQWSVQMEPPVPCHEYDELRPLDAEPCLPGLAFR 1020  
QY 1021 CPVYFROEILVOVIGTLELVGEIEASSMPSLCSLSISFNSSKHHLVGSNASLAQVVMK 1080  
DB 1021 CPVYFROEILVOVIGTLELVGEIEASSMPSLCSLSISFNSSKHHLVGSNASLAQVVMK 1080  
QY 1081 VDVIYKQMLYLYVLSGIGLLILLILFIYLYKVGFFKRNLIKEMKAGRGVPGNIPADS 1140  
DB 1081 VDVIYKQMLYLYVLSGIGLLILLILFIYLYKVGFFKRNLIKEMKAGRGVPGNIPADS 1140  
QY 1141 EQLASGQAGDPGCLKPLHEKXSESGGKD 1170  
DB 1141 EQLASGQAGDPGCLKPLHEKXSESGGKD 1170

RESULT 3  
US-11-080-026-2  
; Sequence 2, Application US/11080026  
; GENERAL INFORMATION:  
; APPLICANT: Springer, Timothy A.  
; APPLICANT: Shimada, Motomu  
; APPLICANT: Lu, Chafen  
; TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A  
; FILE REFERENCE: DESIRED CONFORMATION AND METHODS FOR PRODUCING SAME  
; CURRENT FILING DATE: 2005-03-15  
; PRIOR APPLICATION NUMBER: US/11/080,026  
; PRIOR FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/229,700  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1170  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-080-026-2

Query Match 100.0%; Score 6106; DB 7; Length 1170;  
Best local Similarity 100.0%; Pred. No. 0;  
Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKDSCITMAMALLSGFFFAFPASSYNLDVGCARSFPAPRGRHGVVQLQVGNQVYGA 60  
DB 1 MKDSCITMAMALLSGFFFAFPASSYNLDVGCARSFPAPRGRHGVVQLQVGNQVYGA 60

QY 61 PGBNSTGSLYQCCSGTGHCLPVTLRGSNTSKYLQNTLADPDPDGSLLADPGLSRCTCD 120  
DB 61 PGBNSTGSLYQCCSGTGHCLPVTLRGSNTSKYLQNTLADPDPDGSLLADPGLSRCTCD 120  
QY 121 QNTYLSGLCYLFRONTLOQPMLOGRPGPOECLKGNVLDVFLFDGSMISLOPDSFOKILDPMK 180  
DB 121 QNTYLSGLCYLFRONTLOQPMLOGRPGPOECLKGNVLDVFLFDGSMISLOPDSFOKILDPMK 180  
QY 181 DVMKLSNTSYQFAVOPSTSYKTEPDSYVKKRDPDALIKHYKHMILLTNTGALINYV 240  
DB 181 DVMKLSNTSYQFAVOPSTSYKTEPDSYVKKRDPDALIKHYKHMILLTNTGALINYV 240  
QY 241 ATEVFRBELGARPDATKYLITTDGEATDSGNIDAADKIIRYIIIGIGHFOTKSSQETLH 300  
DB 241 ATEVFRBELGARPDATKYLITTDGEATDSGNIDAADKIIRYIIIGIGHFOTKSSQETLH 300  
QY 301 KPAKSPASEFYKILDTBEKLDLFTLEOKKIYVEGTSKODLTSFNNELSSSGISADLSR 360  
DB 301 KPAKSPASEFYKILDTBEKLDLFTLEOKKIYVEGTSKODLTSFNNELSSSGISADLSR 360  
QY 361 GHAVGAVGADWAGFADLAKADLODDTFIGNEBLTPREVRAGYLYTWTMLPSRQKTSLL 420  
DB 361 GHAVGAVGADWAGFADLAKADLODDTFIGNEBLTPREVRAGYLYTWTMLPSRQKTSLL 420  
QY 421 ASGAPRYQHMGRVILLPOEPQGGHMSOVQTHGTQIGSYFGSELGVVDVDDGETELLII 480  
DB 421 ASGAPRYQHMGRVILLPOEPQGGHMSOVQTHGTQIGSYFGSELGVVDVDDGETELLII 480  
QY 481 GAPIFYGRQGRFITYQORQLGFEVSELOGDGYPGRGGEITLALTDINGGLVDVA 540  
DB 481 GAPIFYGRQGRFITYQORQLGFEVSELOGDGYPGRGGEITLALTDINGGLVDVA 540  
QY 541 VGAPLEBQAVYIENGRRHGLSPQSORIBETQVLSGIQWFGRIHGVKLEGGGLADVA 600  
DB 541 VGAPLEBQAVYIENGRRHGLSPQSORIBETQVLSGIQWFGRIHGVKLEGGGLADVA 600  
QY 601 VQAESOMIVLSRPPVDMVTLMSPSPAPIPVHEVCSTYSNKMKEGVNITTCFOIKSLY 660  
DB 601 VQAESOMIVLSRPPVDMVTLMSPSPAPIPVHEVCSTYSNKMKEGVNITTCFOIKSLY 660  
QY 661 POFQGRUVANLTYTLODGHRTTRRGLPFGGRHRLRNIAVTTSMSCDTSFHFVPCVD 720  
DB 661 POFQGRUVANLTYTLODGHRTTRRGLPFGGRHRLRNIAVTTSMSCDTSFHFVPCVD 720  
QY 721 LISPINVSLNFSLWEEBGTPRDQRAQKDIPIILRPSLSHSETWEIPEKNCGEKCCGAN 780  
DB 721 LISPINVSLNFSLWEEBGTPRDQRAQKDIPIILRPSLSHSETWEIPEKNCGEKCCGAN 780  
QY 781 LRVSPSPARSRLRLTAAPASLSVELSLNLEBDAYVQDLHFPFGLSFRKVENLKPBSQ 840  
DB 781 LRVSPSPARSRLRLTAAPASLSVELSLNLEBDAYVQDLHFPFGLSFRKVENLKPBSQ 840  
QY 841 IPVSCBELPEBSRLSRALSCNVSSPIFKAGHSVALQMMFNTLVNSWGDSEVELHANVTC 900  
DB 841 IPVSCBELPEBSRLSRALSCNVSSPIFKAGHSVALQMMFNTLVNSWGDSEVELHANVTC 900  
QY 901 NNBSDDLLEDSNATITIPILYPINILIDQEDSTLYVSFTPKGPKIHQKMYQVRIQPS 960  
DB 901 NNBSDDLLEDSNATITIPILYPINILIDQEDSTLYVSFTPKGPKIHQKMYQVRIQPS 960  
QY 961 IHDNIPITLEAVGVPOPPSEGPITHQWSVQMEPPVPCHEYDELRPLDAEPCLPGLAFR 1020  
DB 961 IHDNIPITLEAVGVPOPPSEGPITHQWSVQMEPPVPCHEYDELRPLDAEPCLPGLAFR 1020  
QY 1021 CPVYFROEILVOVIGTLELVGEIEASSMPSLCSLSISFNSSKHHLVGSNASLAQVVMK 1080  
DB 1021 CPVYFROEILVOVIGTLELVGEIEASSMPSLCSLSISFNSSKHHLVGSNASLAQVVMK 1080  
QY 1081 VDVIYKQMLYLYVLSGIGLLILLILFIYLYKVGFFKRNLIKEMKAGRGVPGNIPADS 1140  
DB 1081 VDVIYKQMLYLYVLSGIGLLILLILFIYLYKVGFFKRNLIKEMKAGRGVPGNIPADS 1140

RESULT 4  
US-11-107-028-4  
; Sequence 4, Application US/11107028  
; GENERAL INFORMATION:  
; APPLICANT: CHAN, ANDREW C.  
; APPLICANT: GONG, QIAN  
; APPLICANT: MARTIN, FLAVIUS  
; TITLE OF INVENTION: Method for Augmenting B Cell Depletion  
; FILE REFERENCE: P2112R1  
; CURRENT APPLICATION NUMBER: US/11/107,028  
; CURRENT FILING DATE: 2005-04-15  
; PRIOR APPLICATION NUMBER: US 60/563,263  
; PRIOR FILING DATE: 2004-04-16  
; NUMBER OF SEQ ID NOS: 52  
; SEQ ID NO 4  
; LENGTH: 1170  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-107-028-4

Query Match 100.0%; Score 6106; DB 7; Length 1170;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKDSCTTMMAMALLSGFFFPAPASSYNDVNGANSFSPRRGRHGYRVLQVNGVYVGA 60  
DB 1 MKDSCTTMMAMALLSGFFFPAPASSYNDVNGANSFSPRRGRHGYRVLQVNGVYVGA 60  
QY 61 PGEKSTSLKQCCSGTGHCPVTLRGSNTSKYLGMPLADPTDGSILACDPGLSRTCD 120  
DB 61 PGEKSTSLKQCCSGTGHCPVTLRGSNTSKYLGMPLADPTDGSILACDPGLSRTCD 120  
QY 121 QNTYLSGLCYLFRONTLQGPMLQGRPGFQECIKANVDLFLFDGSMSLQPDFQKILDPFK 180  
DB 121 QNTYLSGLCYLFRONTLQGPMLQGRPGFQECIKANVDLFLFDGSMSLQPDFQKILDPFK 180  
QY 181 DVMKLSTSTYQFAA VOSTSTYKTEFPDSYVKKRDPALLKHYKMLLNTTGAINV 240  
DB 181 DVMKLSTSTYQFAA VOSTSTYKTEFPDSYVKKRDPALLKHYKMLLNTTGAINV 240  
QY 241 ATEVFRBELGARPDATKVLIIITDGEATDSGNIDAADIIIRYIIIGIGHFQTKESQETLH 300  
DB 241 ATEVFRBELGARPDATKVLIIITDGEATDSGNIDAADIIIRYIIIGIGHFQTKESQETLH 300  
QY 301 KFAKRPASEFVKILDTPEKLDLFTLEOKKIYVIEGTSKODLTSFNMELSSSGISADISR 360  
DB 301 KFAKRPASEFVKILDTPEKLDLFTLEOKKIYVIEGTSKODLTSFNMELSSSGISADISR 360  
QY 361 GHAVVAGVAGADWAGGFLDLKADLQDDTFIGNBPLTPFVRAGYGYVTWLPSSQKISLL 420  
DB 361 GHAVVAGVAGADWAGGFLDLKADLQDDTFIGNBPLTPFVRAGYGYVTWLPSSQKISLL 420  
QY 421 ASGAPRYOHMGRVLLFOBPQGGHMSOVQTHGTQISYFGSEHCGVUVDDGFEILLI 480  
DB 421 ASGAPRYOHMGRVLLFOBPQGGHMSOVQTHGTQISYFGSEHCGVUVDDGFEILLI 480  
QY 481 GAPLFYGEORGARFYIYORQLGFEVSELQDPCYPLGRFGAITALTDINGDLVVA 540  
DB 481 GAPLFYGEORGARFYIYORQLGFEVSELQDPCYPLGRFGAITALTDINGDLVVA 540  
QY 541 VGAPLEEGAVYINGRHHGLSPQPSORIEGTQVLSGIQWFGSRHGVKLEGGDLADVA 600  
DB 541 VGAPLEEGAVYINGRHHGLSPQPSORIEGTQVLSGIQWFGSRHGVKLEGGDLADVA 600  
QY 601 VGASQMTIVLSSRPVDMVTLMSPPAIPVHEVBCSSTSNKKEGNNITTCQIKSLY 660  
DB 601 VGASQMTIVLSSRPVDMVTLMSPPAIPVHEVBCSSTSNKKEGNNITTCQIKSLY 660

QY 661 POFQGRLVANLTYTLQDGRTRRRGLFPGRRHRLRNIAVTTSMSCTDSPFHPVVCOD 720  
DB 661 POFQGRLVANLTYTLQDGRTRRRGLFPGRRHRLRNIAVTTSMSCTDSPFHPVVCOD 720  
QY 721 LISPINVSINPSLMEEGTFRDQAQCKDIPILRPSLHSEFTWEIPPEKNCGEKCEAN 780  
DB 721 LISPINVSINPSLMEEGTFRDQAQCKDIPILRPSLHSEFTWEIPPEKNCGEKCEAN 780  
QY 781 LRVSPPARARALRLTAPASLVELSLSNLEBDAVWQDLHPFGGLSPFKVEMLKPHSQ 840  
DB 781 LRVSPPARARALRLTAPASLVELSLSNLEBDAVWQDLHPFGGLSPFKVEMLKPHSQ 840  
QY 841 IIVSCBELPRESRLSRALSCNVSSPIFKAGHSVALQMFNTLVNSSWGDVBLHANVC 900  
DB 841 IIVSCBELPRESRLSRALSCNVSSPIFKAGHSVALQMFNTLVNSSWGDVBLHANVC 900  
QY 901 NNEBSDLLEONSATTTIPILYPINILIQODEDSTLYVSPFKPKKHQVHMVQVRQPS 960  
DB 901 NNEBSDLLEONSATTTIPILYPINILIQODEDSTLYVSPFKPKKHQVHMVQVRQPS 960  
QY 961 IHDNIPTEAVVGVPOPPSEGPITHQMSVQMEPPVPCHEDELERLPDAEPCLPGALFR 1020  
DB 961 IHDNIPTEAVVGVPOPPSEGPITHQMSVQMEPPVPCHEDELERLPDAEPCLPGALFR 1020  
QY 1021 CPVVFROEIIIVQVIGTELVGEIBASSMFSLCSLSISFNSSKHFLYGSNASIAQVVMK 1080  
DB 1021 CPVVFROEIIIVQVIGTELVGEIBASSMFSLCSLSISFNSSKHFLYGSNASIAQVVMK 1080  
QY 1081 VDVVYERQMTLYVLSIGILLILLIFLYLVYKVPFKRNLKXKMEGRGVNPGIAPEDS 1140  
DB 1081 VDVVYERQMTLYVLSIGILLILLIFLYLVYKVPFKRNLKXKMEGRGVNPGIAPEDS 1140  
QY 1141 EQLASGOEAGDPGCLKPLHEKDSBSGGKD 1170  
DB 1141 EQLASGOEAGDPGCLKPLHEKDSBSGGKD 1170

RESULT 5  
PCT-US05-02350-653  
; Sequence 653, Application PC/TUS0502350  
; GENERAL INFORMATION:  
; APPLICANT: Ayalon-Soffer, Michal  
; APPLICANT: Levine, Zurit  
; APPLICANT: Sella-Tavor, Osnat  
; APPLICANT: Diber, Alex  
; APPLICANT: Shemesh, Ronen  
; APPLICANT: Toporik, Amir  
; APPLICANT: Rotman, Galit  
; APPLICANT: Nemzer, Sergey  
; APPLICANT: Rosenberg, Avi  
; APPLICANT: Dahary, Dvir  
; APPLICANT: Wool, Assaf  
; APPLICANT: Cojocaru, Gad S.  
; APPLICANT: Akiva, Pinchas  
; APPLICANT: Pollock, Sarah  
; APPLICANT: Savitsky, Kineret  
; APPLICANT: Bernstein, Jeanne  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES ENCODING POLYPEPTIDES AND METHODS USING  
; FILE REFERENCE: 28487  
; CURRENT APPLICATION NUMBER: PCT/US05/02350  
; CURRENT FILING DATE: 2005-02-10  
; NUMBER OF SEQ ID NOS: 1155  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 653  
; LENGTH: 1170  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US05-02350-653

Query Match 99.9%; Score 6098; DB 1; Length 1170;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 MKDSCITVMAMALLSGFFFPAPASSYNLDVGRARSPPRAGRHGRVYLQVNGVIVGA 60
DB 1 MKDSCITVMAMALLSGFFFPAPASSYNLDVGRARSPPRAGRHGRVYLQVNGVIVGA 60
QY 61 PGEAGNSTSLVQCCSGTGHCPLPTLRGNSNTSKYLGMTLATDPTDGSILACDPGLSRTCD 120
DB 61 PGEAGNSTSLVQCCSGTGHCPLPTLRGNSNTSKYLGMTLATDPTDGSILACDPGLSRTCD 120
QY 121 QNTYLSGLCYLFRONLQGPMLQGRPGFQBCIKGNVDVLPFDGSMSLQDPDEFQKILDFPMK 180
DB 121 QNTYLSGLCYLFRONLQGPMLQGRPGFQBCIKGNVDVLPFDGSMSLQDPDEFQKILDFPMK 180
QY 181 DVMKLSTNTSYQFAVQFSTSKTEFDSVYKRDPPALLKHVGMILLNTTFALINVV 240
DB 181 DVMKLSTNTSYQFAVQFSTSKTEFDSVYKRDPPALLKHVGMILLNTTFALINVV 240
QY 241 ATEVERBELGARPDATKVLIIITDGEATDSGNIDAADIIIRYIIGIGHFQTKESQETLH 300
DB 241 ATEVERBELGARPDATKVLIIITDGEATDSGNIDAADIIIRYIIGIGHFQTKESQETLH 300
QY 301 KPASKPASEPVKILDTPEKLDLTELQKIIYIEGTSKODLTSFNMELSSGISADLSR 360
DB 301 KPASKPASEPVKILDTPEKLDLTELQKIIYIEGTSKODLTSFNMELSSGISADLSR 360
QY 361 GHAVVAVGAKDMAGGFLDKADLQDDPTFIGNEBLTPBEVAGYLGATYVWLPSPQKTSLL 420
DB 361 GHAVVAVGAKDMAGGFLDKADLQDDPTFIGNEBLTPBEVAGYLGATYVWLPSPQKTSLL 420
QY 421 ASGARBYOHMGVLLFQEPQGGHWSQVOTIHGTQIGSYFGGELCGVVDQDGETELLII 480
DB 421 ASGARBYOHMGVLLFQEPQGGHWSQVOTIHGTQIGSYFGGELCGVVDQDGETELLII 480
QY 481 GAPLFYGBQGRGVFIYQRRQLGFEEVSELQDPCGYLGRFGAITALTDINGDLVDVA 540
DB 481 GAPLFYGBQGRGVFIYQRRQLGFEEVSELQDPCGYLGRFGAITALTDINGDLVDVA 540
QY 541 VGAPLEEGQAVYIFNGRHGGLSPQSPQRIEGTQVLSGIQWFGRSIHGYKDLBGDLADVA 600
DB 541 VGAPLEEGQAVYIFNGRHGGLSPQSPQRIEGTQVLSGIQWFGRSIHGYKDLBGDLADVA 600
QY 601 VGASEQMTVLSRPVVDWVTLMSFSPARIYHVEVCSYSTSNKMEGVNITTCFOIKSLY 660
DB 601 VGASEQMTVLSRPVVDWVTLMSFSPARIYHVEVCSYSTSNKMEGVNITTCFOIKSLY 660
QY 661 PQFQRLVANTLYTLQDGHRTRRRGLFPGGRHRLRNIAVTTSMCTDFSHPFVQVD 720
DB 661 PQFQRLVANTLYTLQDGHRTRRRGLFPGGRHRLRNIAVTTSMCTDFSHPFVQVD 720
QY 721 LIIPINVSINSLWEEBGPDDQRAQKDIPIILPISLHSTWEIPEEKNGCEDKCEAN 780
DB 721 LIIPINVSINSLWEEBGPDDQRAQKDIPIILPISLHSTWEIPEEKNGCEDKCEAN 780
QY 781 LRVSPSPRSRALRLTAFAISLVELSLNLEEDAWVQDLHFPGLSFRKXEMLKPSHQ 840
DB 781 LRVSPSPRSRALRLTAFAISLVELSLNLEEDAWVQDLHFPGLSFRKXEMLKPSHQ 840
QY 841 IPVSCSELPEBSRLSLRALSQVSSPIFKAGHVALQMMFNTLVSSMGDSVELHANTC 900
DB 841 IPVSCSELPEBSRLSLRALSQVSSPIFKAGHVALQMMFNTLVSSMGDSVELHANTC 900
QY 901 NNBSDDLSDNSATTIIPILYPINILQDQEDSTLYSFTPKGPIKHVKMYQVRIOPS 960
DB 901 NNBSDDLSDNSATTIIPILYPINILQDQEDSTLYSFTPKGPIKHVKMYQVRIOPS 960
QY 961 IHDHNIPTLEAVVGPQPSBGPITHQMSVQMEPPVPCGYEDLELPPAABCPJGALFR 1020
DB 961 IHDHNIPTLEAVVGPQPSBGPITHQMSVQMEPPVPCGYEDLELPPAABCPJGALFR 1020
QY 1021 CPVVEROBILVQVITGLBELVGEIRKASMFSLCSSISIFNSKHFLYGSNLSLAQVVMK 1080
DB 1021 CPVVEROBILVQVITGLBELVGEIRKASMFSLCSSISIFNSKHFLYGSNLSLAQVVMK 1080

```

```

QY 1081 DVVYERKQMLXYLYLSGIGGLLLLLIFLYLYKVFPEKMLKEKMEAGRGVPGICI PAEDS 1140
DB 1081 DVVYERKQMLXYLYLSGIGGLLLLLIFLYLYKVFPEKMLKEKMEAGRGVPGICI PAEDS 1140
QY 1141 EQLASQEGADPGCLKPLHEKDESSEGGKD 1170
DB 1141 EQLASQEGADPGCLKPLHEKDESSEGGKD 1170

RESULT 6
US-09-976-935A-36
; Sequence 36, Application US/0976935A
; GENERAL INFORMATION:
; APPLICANT: Staunton, Donald E.
; TITLE OF INVENTION: MATERIALS AND METHODS TO MODULATE LIGAND BINDING/ENZYMATIC ACTIVI
; FILE REFERENCE: 27866/36470A
; CURRENT APPLICATION NUMBER: US/09/976,935A
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/239,750
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; LENGTH: 1170
; TYPE: PRT
; ORGANISM: amino acid sequence of LFA-1
US-09-976-935A-36

Query Match 99.9%; Score 6098; DB 5; Length 1170;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKDSCITVMAMALLSGFFFPAPASSYNLDVGRARSPPRAGRHGRVYLQVNGVIVGA 60
DB 1 MKDSCITVMAMALLSGFFFPAPASSYNLDVGRARSPPRAGRHGRVYLQVNGVIVGA 60
QY 61 PGEAGNSTSLVQCCSGTGHCPLPTLRGNSNTSKYLGMTLATDPTDGSILACDPGLSRTCD 120
DB 61 PGEAGNSTSLVQCCSGTGHCPLPTLRGNSNTSKYLGMTLATDPTDGSILACDPGLSRTCD 120
QY 121 QNTYLSGLCYLFRONLQGPMLQGRPGFQBCIKGNVDVLPFDGSMSLQDPDEFQKILDFPMK 180
DB 121 QNTYLSGLCYLFRONLQGPMLQGRPGFQBCIKGNVDVLPFDGSMSLQDPDEFQKILDFPMK 180
QY 181 DVMKLSTNTSYQFAVQFSTSKTEFDSVYKRDPPALLKHVGMILLNTTFALINVV 240
DB 181 DVMKLSTNTSYQFAVQFSTSKTEFDSVYKRDPPALLKHVGMILLNTTFALINVV 240
QY 241 ATEVERBELGARPDATKVLIIITDGEATDSGNIDAADIIIRYIIGIGHFQTKESQETLH 300
DB 241 ATEVERBELGARPDATKVLIIITDGEATDSGNIDAADIIIRYIIGIGHFQTKESQETLH 300
QY 301 KPASKPASEPVKILDTPEKLDLTELQKIIYIEGTSKODLTSFNMELSSGISADLSR 360
DB 301 KPASKPASEPVKILDTPEKLDLTELQKIIYIEGTSKODLTSFNMELSSGISADLSR 360
QY 361 GHAVVAVGAKDMAGGFLDKADLQDDPTFIGNEBLTPBEVAGYLGATYVWLPSPQKTSLL 420
DB 361 GHAVVAVGAKDMAGGFLDKADLQDDPTFIGNEBLTPBEVAGYLGATYVWLPSPQKTSLL 420
QY 421 ASGARBYOHMGVLLFQEPQGGHWSQVOTIHGTQIGSYFGGELCGVVDQDGETELLII 480
DB 421 ASGARBYOHMGVLLFQEPQGGHWSQVOTIHGTQIGSYFGGELCGVVDQDGETELLII 480
QY 481 GAPLFYGBQGRGVFIYQRRQLGFEEVSELQDPCGYLGRFGAITALTDINGDLVDVA 540
DB 481 GAPLFYGBQGRGVFIYQRRQLGFEEVSELQDPCGYLGRFGAITALTDINGDLVDVA 540
QY 541 VGAPLEEGQAVYIFNGRHGGLSPQSPQRIEGTQVLSGIQWFGRSIHGYKDLBGDLADVA 600
DB 541 VGAPLEEGQAVYIFNGRHGGLSPQSPQRIEGTQVLSGIQWFGRSIHGYKDLBGDLADVA 600

```

Qy 601 VGASQMIIVLSRPVDMVTLMSPAEIPVHEVECSYSTSNKMGVNTTICFOIKSLY 660  
Db 601 VGASQMIIVLSRPVDMVTLMSPAEIPVHEVECSYSTSNKMGVNTTICFOIKSLY 660  
Qy 661 POFQGRIVANLTYTLQDGHRTTRRGLPFGGRHELRNIAVTTSMSCDPSFHPVCYOD 720  
Db 661 POFQGRIVANLTYTLQDGHRTTRRGLPFGGRHELRNIAVTTSMSCDPSFHPVCYOD 720  
Qy 721 LISPIVNSLNFSLMBEETPRDQRAQKDIPIILRPSLSHETWEIPFEKNGGDKCEAN 780  
Db 721 LISPIVNSLNFSLMBEETPRDQRAQKDIPIILRPSLSHETWEIPFEKNGGDKCEAN 780  
Qy 781 LRVSPSPARARLRTAFASLSVELSLNLEBDAYWQDLHFPFGLSFRKVENLKPMSQ 840  
Db 781 LRVSPSPARARLRTAFASLSVELSLNLEBDAYWQDLHFPFGLSFRKVENLKPMSQ 840  
Qy 841 IPVSCBELPEESRLSRALSQVSSPIFKAGHSVALQMMFNTLVNNSWGDSEVELHANVTC 900  
Db 841 IPVSCBELPEESRLSRALSQVSSPIFKAGHSVALQMMFNTLVNNSWGDSEVELHANVTC 900  
Qy 901 NNESSLLEEDNSATTIIPILYPINILIDQEDSTLYVSTFKPGPKIHQVKHMYOVR1OPS 960  
Db 901 NNESSLLEEDNSATTIIPILYPINILIDQEDSTLYVSTFKPGPKIHQVKHMYOVR1OPS 960  
Qy 961 IHDNIPITLBAVGVQPPSEBGPITTHQWSVQMEPPVPCHVEDLERLPDAEPCLPGALFR 1020  
Db 961 IHDNIPITLBAVGVQPPSEBGPITTHQWSVQMEPPVPCHVEDLERLPDAEPCLPGALFR 1020  
Qy 1021 CPVYFRQELIVQVIGTLELVEIEIASMFSLCSSLSISFNSSKIFHLVGSNASTLAQVYMK 1080  
Db 1021 CPVYFRQELIVQVIGTLELVEIEIASMFSLCSSLSISFNSSKIFHLVGSNASTLAQVYMK 1080  
Qy 1081 VDVIYKEMQLTYLYLSGIGLLLLPIVLKYKGFYKRNLEKMEAGRGVPGNIPADS 1140  
Db 1081 VDVIYKEMQLTYLYLSGIGLLLLPIVLKYKGFYKRNLEKMEAGRGVPGNIPADS 1140  
Qy 1141 EQLASQGEAGDPGCLKPLHEKDSGSGGKD 1170  
Db 1141 EQLASQGEAGDPGCLKPLHEKDSGSGGKD 1170

RESULT 7  
US-11-043-770-653  
; Sequence 653, Application US/11043770  
; GENERAL INFORMATION:  
; APPLICANT: Ayalon-Soffer, Michal  
; APPLICANT: Levine, Zuric  
; APPLICANT: Sella-Tavor, Osnat  
; APPLICANT: Diber, Alex  
; APPLICANT: Shemesh, Ronen  
; APPLICANT: Toporik, Amir  
; APPLICANT: Rotman, Galit  
; APPLICANT: Nemzer, Sergey  
; APPLICANT: Rosenberg, Avi  
; APPLICANT: Dahanay, Dvir  
; APPLICANT: Wool, Asaaf  
; APPLICANT: Cojocaru, Gad S.  
; APPLICANT: Pollock, Sarah  
; APPLICANT: Savitsky, Kineret  
; APPLICANT: Bernstejn, Jeanne  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES ENCODING POLYPEPTIDES AND METHODS USING  
; FILE REFERENCE: 28488  
; CURRENT APPLICATION NUMBER: US/11/043,770  
; CURRENT FILING DATE: 2005-01-27  
; NUMBER OF SEQ ID NOS: 1155  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 653  
; LENGTH: 1170  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-043-770-653

Query Match 99.9%; Score 6098; DB 7; Length 1170;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1163; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKDSCITVAMALLSGFFPAPASSYNDVGRARSFPSPAPGHPGVRVLQVANGVIVA 60  
Db 1 MKDSCITVAMALLSGFFPAPASSYNDVGRARSFPSPAPGHPGVRVLQVANGVIVA 60  
Qy 61 PGEKNGTSGSLYQOQSGHCLPTVTLRGSNTSRYLQMTLATDPTDGSILA CDGLSRTCD 120  
Db 61 PGEKNGTSGSLYQOQSGHCLPTVTLRGSNTSRYLQMTLATDPTDGSILA CDGLSRTCD 120  
Qy 121 QNTYLSGLCYLFRONLOGPMLQGRPGFOECIKGNVDVLFPLDSMSLQDPFOKILDFPMK 180  
Db 121 QNTYLSGLCYLFRONLOGPMLQGRPGFOECIKGNVDVLFPLDSMSLQDPFOKILDFPMK 180  
Qy 181 DVMKKLSNTSYQFAAVQFSTSYKTEPFDSDYVRKDPDALLKHKVKMLLTNTFGA1NVY 240  
Db 181 DVMKKLSNTSYQFAAVQFSTSYKTEPFDSDYVRKDPDALLKHKVKMLLTNTFGA1NVY 240  
Qy 241 ATEVFREELGARPDATVULIITDGEATDSGNIDAAKDIIRYIIGIKHFOQTESOETLH 300  
Db 241 ATEVFREELGARPDATVULIITDGEATDSGNIDAAKDIIRYIIGIKHFOQTESOETLH 300  
Qy 301 KFASKPASEFVKLIDPFEKLDLFTLEOKKIYIEGTSKODLTSFNMELSSSGISADLSR 360  
Db 301 KFASKPASEFVKLIDPFEKLDLFTLEOKKIYIEGTSKODLTSFNMELSSSGISADLSR 360  
Qy 361 GHAVVAGVAKDWAAGFLDLKADLQDDTFIGNEPLTPEVAVAGLYGTVTMLPSRQKTSLL 420  
Db 361 GHAVVAGVAKDWAAGFLDLKADLQDDTFIGNEPLTPEVAVAGLYGTVTMLPSRQKTSLL 420  
Qy 421 ASGAPRYQHMGVRLPQEPQGGHMSOVOTIHOTQIGSYVSGELCGVDVQDDETELLI 480  
Db 421 ASGAPRYQHMGVRLPQEPQGGHMSOVOTIHOTQIGSYVSGELCGVDVQDDETELLI 480  
Qy 481 GAPLFYGEORQGVFIYQRRQLGFEVEYSELQDPGYLGRFGA1TALTDINDGLVDVA 540  
Db 481 GAPLFYGEORQGVFIYQRRQLGFEVEYSELQDPGYLGRFGA1TALTDINDGLVDVA 540  
Qy 541 VGAPLEBQGA1VYIPNGRHGSLSPQPSORIIGTOVLSGIQMFGRS1HGVDLBSGD1ADVA 600  
Db 541 VGAPLEBQGA1VYIPNGRHGSLSPQPSORIIGTOVLSGIQMFGRS1HGVDLBSGD1ADVA 600  
Qy 601 VGASQMIIVLSRPVDMVTLMSPAEIPVHEVECSYSTSNKMGVNTTICFOIKSLY 660  
Db 601 VGASQMIIVLSRPVDMVTLMSPAEIPVHEVECSYSTSNKMGVNTTICFOIKSLY 660  
Qy 661 POFQGRIVANLTYTLQDGHRTTRRGLPFGGRHELRNIAVTTSMSCDPSFHPVCYOD 720  
Db 661 POFQGRIVANLTYTLQDGHRTTRRGLPFGGRHELRNIAVTTSMSCDPSFHPVCYOD 720  
Qy 721 LISPIVNSLNFSLMBEETPRDQRAQKDIPIILRPSLSHETWEIPFEKNGGDKCEAN 780  
Db 721 LISPIVNSLNFSLMBEETPRDQRAQKDIPIILRPSLSHETWEIPFEKNGGDKCEAN 780  
Qy 781 LRVSPSPARARLRTAFASLSVELSLNLEBDAYWQDLHFPFGLSFRKVENLKPMSQ 840  
Db 781 LRVSPSPARARLRTAFASLSVELSLNLEBDAYWQDLHFPFGLSFRKVENLKPMSQ 840  
Qy 841 IPVSCBELPEESRLSRALSQVSSPIFKAGHSVALQMMFNTLVNNSWGDSEVELHANVTC 900  
Db 841 IPVSCBELPEESRLSRALSQVSSPIFKAGHSVALQMMFNTLVNNSWGDSEVELHANVTC 900  
Qy 901 NNESSLLEEDNSATTIIPILYPINILIDQEDSTLYVSTFKPGPKIHQVKHMYOVR1OPS 960  
Db 901 NNESSLLEEDNSATTIIPILYPINILIDQEDSTLYVSTFKPGPKIHQVKHMYOVR1OPS 960  
Qy 961 IHDNIPITLBAVGVQPPSEBGPITTHQWSVQMEPPVPCHVEDLERLPDAEPCLPGALFR 1020  
Db 961 IHDNIPITLBAVGVQPPSEBGPITTHQWSVQMEPPVPCHVEDLERLPDAEPCLPGALFR 1020



QY 1021 CPVVFROEILVQVIGTLELVEIBASSNFSLCSLSISFNSSKHFHLYGSNASTLAQVVMK 1080  
DB 1021 CPVVFROEILVQVIGTLELVEIBASSNFSLCSLSISFNSSKHFHLYGSNASTLAQVVMK 1080  
QY 1081 VDVFYKQMLLYLVLSGIGGLLLLLLFYLVYKVFGRNLIKEMAGRGVPGNGIPAEBS 1140  
DB 1081 VDVFYKQMLLYLVLSGIGGLLLLLLFYLVYKVFGRNLIKEMAGRGVPGNGIPAEBS 1140  
QY 1141 EQLASGQAGDPGCLKPLHKKDSGSGGKD 1170  
DB 1141 EQLASGQAGDPGCLKPLHKKDSGSGGKD 1170

## RESULT 8

US-11-062-290-1  
Sequence 1, Application US/11062290  
GENERAL INFORMATION:  
APPLICANT: KAPUSTAY, PAMELA M.  
APPLICANT: LEWIS, REX H.  
TITLE OF INVENTION: LPA-1 ALPHA SUBUNIT ANTIBODIES AND METHODS OF USE  
FILE REFERENCE: 046007/0272304  
CURRENT APPLICATION NUMBER: US/11/062, 290  
CURRENT FILING DATE: 2005-02-17  
PRIOR APPLICATION NUMBER: US/10/261,164  
PRIOR FILING DATE: 2002-09-27  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 1  
LENGTH: 1170  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-062-290-1

Query Match 99.9%; Score 6098; DB 7; Length 1170;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKDSCITVMAMALLSGFFFPAPASSYNLDVKGASFPSPRAGRHFGRVLOVNGVYGA 60  
DB 1 MKDSCITVMAMALLSGFFFPAPASSYNLDVKGASFPSPRAGRHFGRVLOVNGVYGA 60  
QY 61 PGBNSNSTSLYQCCSGTGHCPLVTLRGSNYSKYLGMFLADPTDGSILACDPGLSRTCD 120  
DB 61 PGBNSNSTSLYQCCSGTGHCPLVTLRGSNYSKYLGMFLADPTDGSILACDPGLSRTCD 120  
QY 121 QNTYLSGLCYLFRONTLQSPMLQGRPGQECIKGNVDLFLFDGSMISLPDEFQKILDFPMK 180  
DB 121 QNTYLSGLCYLFRONTLQSPMLQGRPGQECIKGNVDLFLFDGSMISLPDEFQKILDFPMK 180  
QY 181 DVNKKLSTNTSYQFAAVQSTSYKTEPDSYVKRDPDALLKHYKMLLTNTFGAINVY 240  
DB 181 DVNKKLSTNTSYQFAAVQSTSYKTEPDSYVKRDPDALLKHYKMLLTNTFGAINVY 240  
QY 241 ATYVREBELGARPRATKYLIIITDGEATDSGNIDAADIIVYIGIGHFQTKESQETLH 300  
DB 241 ATYVREBELGARPRATKYLIIITDGEATDSGNIDAADIIVYIGIGHFQTKESQETLH 300  
QY 301 KFASKPASEFYKIDTFEKLKDLFTELQKTYVEGTSKODLTSFNNELSSGASADLSR 360  
DB 301 KFASKPASEFYKIDTFEKLKDLFTELQKTYVEGTSKODLTSFNNELSSGASADLSR 360  
QY 361 GHAVVAVGAKDMWAGFLDLKADLDDTFIGNEPILTEPVAAGYLYGYTVMPLPSRQKTSLL 420  
DB 361 GHAVVAVGAKDMWAGFLDLKADLDDTFIGNEPILTEPVAAGYLYGYTVMPLPSRQKTSLL 420  
QY 421 ASGAPRYOHMRVLLFQEPQGGHMSQVTHHGTIGISYFGSELGVVDDDGTELLLI 480  
DB 421 ASGAPRYOHMRVLLFQEPQGGHMSQVTHHGTIGISYFGSELGVVDDDGTELLLI 480  
QY 481 GAPLFYGBQSGRGRVYIYORQLGFEVSELQDPCGYPLGRGGAITALTIDNGGLVDVA 540  
DB 481 GAPLFYGBQSGRGRVYIYORQLGFEVSELQDPCGYPLGRGGAITALTIDNGGLVDVA 540

QY 541 VGAPLEBOGAVYIFNGHGLSPQSPQRIBGTQVLSGIQWFGSHIGVKDLBEGDLADVA 600  
DB 541 VGAPLEBOGAVYIFNGHGLSPQSPQRIBGTQVLSGIQWFGSHIGVKDLBEGDLADVA 600  
QY 601 VGASQMTIVLSRPVDMVTLMSRPAEIPVHEVECSYSTSNKKGSGNITTCFOIKSLY 660  
DB 601 VGASQMTIVLSRPVDMVTLMSRPAEIPVHEVECSYSTSNKKGSGNITTCFOIKSLY 660  
QY 661 PQQGRVLANVLTLODGHRTRRRGLFGRRHRLRNIAVTTSMSTDSFHPVPCVD 720  
DB 661 PQQGRVLANVLTLODGHRTRRRGLFGRRHRLRNIAVTTSMSTDSFHPVPCVD 720  
QY 721 LISPIVSLNPSLMBEETPRDQAOCKDIPILRPSLSETBWIPERKCGEDKCEAN 780  
DB 721 LISPIVSLNPSLMBEETPRDQAOCKDIPILRPSLSETBWIPERKCGEDKCEAN 780  
QY 781 LRVSPSARARALRTAFASLVELSISNLEDAVYVQDLHPPGSLFRKVEMLKPSQ 840  
DB 781 LRVSPSARARALRTAFASLVELSISNLEDAVYVQDLHPPGSLFRKVEMLKPSQ 840  
QY 841 IPVSCBELPERSRLSRALSCNVSPIFKAGSHVALQMMNTLVNSWGDVVELHANVTC 900  
DB 841 IPVSCBELPERSRLSRALSCNVSPIFKAGSHVALQMMNTLVNSWGDVVELHANVTC 900  
QY 901 NNEDSDLENSATTTIPILPINILIQDQEDSTLYVFTPKGPKHQVKNTOVRLOPS 960  
DB 901 NNEDSDLENSATTTIPILPINILIQDQEDSTLYVFTPKGPKHQVKNTOVRLOPS 960  
QY 961 IHDNIPTELVAVGVPPQSEGPITTHQMSVQMEPPVPCHEDELRPLDPAEPCPLGALFR 1020  
DB 961 IHDNIPTELVAVGVPPQSEGPITTHQMSVQMEPPVPCHEDELRPLDPAEPCPLGALFR 1020  
QY 1021 CPVVFROEILVQVIGTLELVEIBASSNFSLCSLSISFNSSKHFHLYGSNASTLAQVVMK 1080  
DB 1021 CPVVFROEILVQVIGTLELVEIBASSNFSLCSLSISFNSSKHFHLYGSNASTLAQVVMK 1080  
QY 1081 VDVFYKQMLLYLVLSGIGGLLLLLLFYLVYKVFGRNLIKEMAGRGVPGNGIPAEBS 1140  
DB 1081 VDVFYKQMLLYLVLSGIGGLLLLLLFYLVYKVFGRNLIKEMAGRGVPGNGIPAEBS 1140  
QY 1141 EQLASGQAGDPGCLKPLHKKDSGSGGKD 1170  
DB 1141 EQLASGQAGDPGCLKPLHKKDSGSGGKD 1170

## RESULT 9

PCT-US03-10870-295  
Sequence 295, Application PC/TUS0310870  
GENERAL INFORMATION:  
APPLICANT: Mitokor, Inc.  
APPLICANT: Buck Institute  
APPLICANT: Ghosh, Soumitra S.  
APPLICANT: Fahy, Eoin D.  
APPLICANT: Zhang, Bing  
APPLICANT: Gibson, Bradford W.  
APPLICANT: Taylor, Steven W.  
APPLICANT: Glenn, Gary M.  
APPLICANT: Warnock, Dale B.  
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
FILE REFERENCE: 660088.465PC  
CURRENT APPLICATION NUMBER: PCT/US03/10870  
CURRENT FILING DATE: 2003-04-04  
NUMBER OF SEQ ID NOS: 3025  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 295  
LENGTH: 1223  
TYPE: PRT  
ORGANISM: Homo sapiens  
PCT-US03-10870-295

Query Match 99.1%; Score 6053.5; DB 1; Length 1223;  
Best Local Similarity 95.5%; Pred. No. 0;

Matches 1168; Conservative 0; Mismatches 2; Indels 53; Gaps 1;

QY 1 MKDSCITMAMALLSGFFFPASSYNLDVARGSPSPRAGRHRGVYLVQNGVYGA 60  
DB 1 MKDSCITMAMALLSGFFFPASSYNLDVARGSPSPRAGRHRGVYLVQNGVYGA 60  
QY 61 PGBGNSTSLYQCSGTHCLPVTLRGNSYTSKYLGMTATDPTDGSILACDPGLSRTCD 120  
DB 61 PGBGNSTSLYQCSGTHCLPVTLRGNSYTSKYLGMTATDPTDGSILACDPGLSRTCD 120  
QY 121 QNTYLSGICITFRONLQGPMLQGRPGFOECIKGNVDVLFPLDGSMSLQDPDEFQKILDPMK 180  
DB 121 QNTYLSGICITFRONLQGPMLQGRPGFOECIKGNVDVLFPLDGSMSLQDPDEFQKILDPMK 180  
QY 181 DVMKCLSTSYQFAVQSTSYKTEPFDSVYKRRDPALLKHVKNMILLNTGAINVY 240  
DB 181 DVMKCLSTSYQFAVQSTSYKTEPFDSVYKRRDPALLKHVKNMILLNTGAINVY 240  
QY 241 ATEVFRBELGARPDATKVLIIITDGEATDSGNIDAADKIIRYIIGIGHFQTKESQETLH 300  
DB 241 ATEVFRBELGARPDATKVLIIITDGEATDSGNIDAADKIIRYIIGIGHFQTKESQETLH 300  
QY 301 KFAKSPASEFYKILDTPEKLDLFTLEOKIYVIEGTSKODLTSENMELSSSGISADLSR 360  
DB 301 KFAKSPASEFYKILDTPEKLDLFTLEOKIYVIEGTSKODLTSENMELSSSGISADLSR 360  
QY 361 GHAVVGAAGAKMAGGFLDLKADLQDDPFIGNEPTEPVRAGYGYTWTMLPSRQKSTLL 420  
DB 361 GHAVVGAAGAKMAGGFLDLKADLQDDPFIGNEPTEPVRAGYGYTWTMLPSRQKSTLL 420  
QY 421 ASGARPYQOMGRVLLFOEPQGGHMSQVOTIHGTQIGSYFGSELGVVDODGETELLII 480  
DB 421 ASGARPYQOMGRVLLFOEPQGGHMSQVOTIHGTQIGSYFGSELGVVDODGETELLII 480  
QY 481 GARPFGYQGRGRFYIYORROLGFEVESELQDPEGYLGRFGEAITALTINDGVLVDA 540  
DB 481 GARPFGYQGRGRFYIYORROLGFEVESELQDPEGYLGRFGEAITALTINDGVLVDA 540  
QY 541 VGAPLEBQAGAYYINRHRGHSPOPSQIEGTQVLSGIQWGRSRHGVKLEGGGLADVA 600  
DB 541 VGAPLEBQAGAYYINRHRGHSPOPSQIEGTQVLSGIQWGRSRHGVKLEGGGLADVA 600  
QY 601 VGASQOMIVLSRPVDMVTLMSFSPARIPIVHEVCSYSTSNKMEGVNITICFOIKSLY 660  
DB 601 VGASQOMIVLSRPVDMVTLMSFSPARIPIVHEVCSYSTSNKMEGVNITICFOIKSLY 660  
QY 661 POFQGRIVANITLYTLOLDHRTRRRGLPGRGHELRNNIAVTTSMCTDFSFPHPVCYQD 720  
DB 661 POFQGRIVANITLYTLOLDHRTRRRGLPGRGHELRNNIAVTTSMCTDFSFPHPVCYQD 720  
QY 721 LISPIVNSLNSLMBEESTPRDORAQKDIPIILRPSLSHRTWIRPEKNGGDEKCKCAN 780  
DB 721 LISPIVNSLNSLMBEESTPRDORAQKDIPIILRPSLSHRTWIRPEKNGGDEKCKCAN 780  
QY 781 LRVFSFSPARSRLNLTAFAASVLSLSNLEBDAYWVOLDLHFPFGLSFRKYEMLKPHSQ 840  
DB 781 LRVFSFSPARSRLNLTAFAASVLSLSNLEBDAYWVOLDLHFPFGLSFRKYEMLKPHSQ 840  
QY 841 IPVSCBELPEBSRLISRLSCNVSSPIFKAGHSVALQMMFNTLVNSSGDSEVELHANVC 900  
DB 841 IPVSCBELPEBSRLISRLSCNVSSPIFKAGHSVALQMMFNTLVNSSGDSEVELHANVC 900  
QY 901 NNEGSDILLENSATTTIPIILPINILLQDQEDSTLYSFTPKGPIHGVKNMYC----- 954  
DB 901 NNEGSDILLENSATTTIPIILPINILLQDQEDSTLYSFTPKGPIHGVKNMYC----- 954  
QY 955 -----VRIQPSIHDHNP 967  
DB 955 -----VRIQPSIHDHNP 967  
QY 961 EMQTSKOTLCRPAQDAHTVGAQGECLPCPWGVSEARFNDNIRAGCRKRIRIOPSHDNIP 1020  
DB 961 EMQTSKOTLCRPAQDAHTVGAQGECLPCPWGVSEARFNDNIRAGCRKRIRIOPSHDNIP 1020  
QY 968 TLBAVGVGPDPSSGPITTHQMSVQMEPPVPCHYBDELRLLPDAABCLPFGALFRCPVVRQ 1027  
DB 968 TLBAVGVGPDPSSGPITTHQMSVQMEPPVPCHYBDELRLLPDAABCLPFGALFRCPVVRQ 1027  
QY 1021 TLBAVGVGPDPSSGPITTHQMSVQMEPPVPCHYBDELRLLPDAABCLPFGALFRCPVVRQ 1080  
DB 1021 TLBAVGVGPDPSSGPITTHQMSVQMEPPVPCHYBDELRLLPDAABCLPFGALFRCPVVRQ 1080

QY 1028 EILVQVITGLTLYGEIRASMSFSLCSLSISFNSSKHFLHYGSNASLAQVVMKVYVER 1087  
DB 1081 EILVQVITGLTLYGEIRASMSFSLCSLSISFNSSKHFLHYGSNASLAQVVMKVYVER 1140  
QY 1088 QMLYLYLSGIGILLLLLLIFIVLYKVFPRKMLKEMMEAGRVNPGIPADESEQLASQ 1147  
DB 1141 QMLYLYLSGIGILLLLLLIFIVLYKVFPRKMLKEMMEAGRVNPGIPADESEQLASQ 1200  
QY 1148 EAGDPGLKRLHEDSSGGGKD 1170  
DB 1201 EAGDPGLKRLHEDSSGGGKD 1223

RESULT 10  
US-11-021-951-130  
Sequence 130, Application US/11021951  
GENERAL INFORMATION:  
APPLICANT: HAUPTS, Ulrich  
APPLICANT: KOLTERMANN, Andre  
APPLICANT: SCHREIDIG, Andreas  
APPLICANT: VOTSMETTER, Christian  
APPLICANT: Ketting, Ulrich  
APPLICANT: COCO, Wayne Michael  
TITLE OF INVENTION: New Biological Entities And The Pharmaceutical  
FILE REFERENCE: 04156.000205  
CURRENT APPLICATION NUMBER: US/11/021.951  
CURRENT FILING DATE: 2004-12-22  
PRIOR APPLICATION NUMBER: 10/872.198  
PRIOR FILING DATE: 2004-06-18  
PRIOR APPLICATION NUMBER: 60/543.518  
PRIOR FILING DATE: 2004-02-11  
PRIOR APPLICATION NUMBER: 60/524.960  
PRIOR FILING DATE: 2003-11-25  
PRIOR APPLICATION NUMBER: EP 04003058  
PRIOR FILING DATE: 2004-02-11  
PRIOR APPLICATION NUMBER: EP 03025871  
PRIOR FILING DATE: 2003-11-11  
PRIOR APPLICATION NUMBER: EP 03025851  
PRIOR FILING DATE: 2003-11-10  
PRIOR APPLICATION NUMBER: EP 03013819  
NUMBER OF SEQ ID NOS: 191  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 130  
LENGTH: 1145  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-021-951-130

Query Match 98.0%; Score 5981; DB 7; Length 1145;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 YNLDVARGSPSPRAGRHRGVYLVQNGVYIGAPGEBGNSSTSLYQCSGTHCLPVTL 85  
DB 1 YNLDVARGSPSPRAGRHRGVYLVQNGVYIGAPGEBGNSSTSLYQCSGTHCLPVTL 60  
QY 86 RGSNYTSKYLGMTLATDPTDGSILACDPGLSRTCDQNTYLSGICITFRONLQGPMLQGRP 145  
DB 61 RGSNYTSKYLGMTLATDPTDGSILACDPGLSRTCDQNTYLSGICITFRONLQGPMLQGRP 120  
QY 146 GFQECIKGNVDVLFPLDGSMSLQDPDEFQKILDPMKQVMKLSNTSYQFAVQSTSYKTE 205  
DB 121 GFQECIKGNVDVLFPLDGSMSLQDPDEFQKILDPMKQVMKLSNTSYQFAVQSTSYKTE 180  
QY 206 FDSQDYKRRDOPALLKHVKNMILLNTGAINVVAITEVFRBELGARPDATKVLIIITDGS 265  
DB 181 FDSQDYKRRDOPALLKHVKNMILLNTGAINVVAITEVFRBELGARPDATKVLIIITDGS 240  
QY 266 EATDSGNIDAADKIIRYIIGIGHFQTKESQETLHFKASAPASEFYKILDTPEKLDLFT 325  
DB 266 EATDSGNIDAADKIIRYIIGIGHFQTKESQETLHFKASAPASEFYKILDTPEKLDLFT 325

Db 241 EATSDGNDAADIIIRYIIIGIKHQTKESQETLHKFKASKPASEVVKILDTREKLDLPT 300  
Qy 336 ELQKKIYIIEGTSKODLTSFNNELSSSGISADLSRGHVAVGAKDWAAGFLLDKADLQ 385  
Db 301 ELQKKIYIIEGTSKODLTSFNNELSSSGISADLSRGHVAVGAKDWAAGFLLDKADLQ 360  
Qy 366 DDTFIGNELTPEVPAQYIGYVTVWLPSRQKTSLLASGAPRYQHNKRVLLFQEPQGGHW 445  
Db 361 DDTFIGNELTPEVPAQYIGYVTVWLPSRQKTSLLASGAPRYQHNKRVLLFQEPQGGHW 420  
Qy 446 SOVQIHGQISYSGELCGVDVDDGETELLIGAPFYEGQGRGFYIQRQLGPE 505  
Db 421 SOVQIHGQISYSGELCGVDVDDGETELLIGAPFYEGQGRGFYIQRQLGPE 480  
Qy 506 EVSEIQDPCGYPLGFGGALITALTIDNGDLVDAVGAAPLEQAGVYIFNGRHGGLSPQ 565  
Db 481 EVSEIQDPCGYPLGFGGALITALTIDNGDLVDAVGAAPLEQAGVYIFNGRHGGLSPQ 540  
Qy 566 SQRIEGTQVLSGIQWFGRSIHGVKDLBGGDLADVAVGAESQMI VLSRPVDMVTLMSPS 625  
Db 541 SQRIEGTQVLSGIQWFGRSIHGVKDLBGGDLADVAVGAESQMI VLSRPVDMVTLMSPS 600  
Qy 626 PABIVHVEECYSYTSNNKKEGVNITTCQIKSLYPOFGRLVANLTYTLQDGHRTRR 685  
Db 601 PABIVHVEECYSYTSNNKKEGVNITTCQIKSLYPOFGRLVANLTYTLQDGHRTRR 660  
Qy 666 GLPFGGRHRLRNIAVTTSMSCDPSFHPVPCVODLISPINVS LPSLMBEERTPRDRA 745  
Db 661 GLPFGGRHRLRNIAVTTSMSCDPSFHPVPCVODLISPINVS LPSLMBEERTPRDRA 720  
Qy 746 QGKDIPIILRPSLHSETWEIPEKNCGEDKCCANLRSFSPARSALRLTAFASLVEL 805  
Db 721 QGKDIPIILRPSLHSETWEIPEKNCGEDKCCANLRSFSPARSALRLTAFASLVEL 780  
Qy 806 SLNSLEBDAYVQDLHFRPPGLSPKVEMLKPHSQIPVSCBELPEESRLLSALSCNVSS 865  
Db 781 SLNSLEBDAYVQDLHFRPPGLSPKVEMLKPHSQIPVSCBELPEESRLLSALSCNVSS 840  
Qy 866 PLFKAGHVALQOMENTLVNSSWGDSVELHANVTGNEDSDLEBNSATITIPILYPINI 925  
Db 841 PLFKAGHVALQOMENTLVNSSWGDSVELHANVTGNEDSDLEBNSATITIPILYPINI 900  
Qy 926 LIQDQEDSTLYVSTFPKGPRIHQVGMQVRIQPSIHDHNIPTLEAVVGVPOPSBEGIT 985  
Db 901 LIQDQEDSTLYVSTFPKGPRIHQVGMQVRIQPSIHDHNIPTLEAVVGVPOPSBEGIT 960  
Qy 986 HQMSVQMBPVPCHYEDLERLPDAAPCLPGALFRCPVFRQELIVQVIGTLELVEGEIEA 1045  
Db 961 HQMSVQMBPVPCHYEDLERLPDAAPCLPGALFRCPVFRQELIVQVIGTLELVEGEIEA 1020  
Qy 1046 SSMFSLCSSLISFNSSKHFLYGSNASTLAQVVMKRVVYERKOML YLYVLSIGLILL 1105  
Db 1021 SSMFSLCSSLISFNSSKHFLYGSNASTLAQVVMKRVVYERKOML YLYVLSIGLILL 1080  
Qy 1106 LIFFILYVYKGFPRKULKEKMBAGRGVNGIIPADESBOLASGEADPGCLRHKESDES 1165  
Db 1081 LIFFILYVYKGFPRKULKEKMBAGRGVNGIIPADESBOLASGEADPGCLRHKESDES 1140  
Qy 1166 GGGKD 1170  
Db 1141 GGGKD 1145

RESULT 11  
PCT-US03-10870-1871  
; Sequence 1871, Application PC/TUS0310870  
; GENERAL INFORMATION:

; APPLICANT: Mitokor, Inc.  
; APPLICANT: Buck Institute  
; APPLICANT: Ghosh, Soumitra S.  
; APPLICANT: Fahy, Bojin D.  
; APPLICANT: Zhang, Bing  
; APPLICANT: Gibson, Bradford W.

; APPLICANT: Taylor, Steven W.  
; APPLICANT: Glenn, Gary M.  
; APPLICANT: Marnock, Dale E.  
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME  
; FILE REFERENCE: 660088.465PC  
; CURRENT APPLICATION NUMBER: PCT/US03/10870  
; NUMBER OF SEQ ID NOS: 2003-04-04  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 1871  
; LENGTH: 1086  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US03-10870-1871

Query Match 91.5%; Score 5585; DB 1; Length 1086;  
Best Local Similarity 92.7%; Pred. No. 0;  
Matches 1085; Conservative 0; Mismatches 1; Indels 84; Gaps 2;

Qy 1 MKDSCITVMAALSGFFFPAPASSYNDVARGASFPSPRAGRHYRVLVQNGVYIGA 60  
Db 1 MKDSCITVMAALSGFFFPAPASSYNDVARGASFPSPRAGRHYRVLVQNGVYIGA 60  
Qy 61 PEGNSTGSLYQCSGTGHCPLVTLRGSNTSKYLGMTLATDPTDGLACDPGLSRYCD 120  
Db 61 PEGNSTGSLYQCSGTGHCPLVTLRGSNTSKYLGMTLATDPTDGLACDPGLSRYCD 109  
Qy 121 QNTYLSGLCYLFRONLQGPMLQGRPGQECIKGNVDLVFLPDSGMSLOPDEFQKIDPMK 180  
Db 110 ----- 109  
Qy 181 DVMKKLSNTSYQFAAVQESTSYKTEPESDVYKRDPAALIKHYKHMILLTNTGATINYV 240  
Db 110 -----FAAVQFSTSYKTEPESDVYKRDPAALIKHYKHMILLTNTGATINYV 157  
Qy 241 ATEVFERELGARPATKYLIIITDGEATDSNIDAADIIIRYIIIGIKHQTKESQETLH 300  
Db 158 ATEVFERELGARPATKYLIIITDGEATDSNIDAADIIIRYIIIGIKHQTKESQETLH 217  
Qy 301 KFAKAPABEFYKIIDTEKLDLFTLEOKKIYIIEGTSKODLTSFNNELSSSGISADLSR 360  
Db 218 KFAKAPABEFYKIIDTEKLDLFTLEOKKIYIIEGTSKODLTSFNNELSSSGISADLSR 277  
Qy 361 GHAVVGAAGADWAGGFLDLKADLQDPTFIGNELTPEVPAQYIGYVTVWLPSRQKTSLL 420  
Db 278 GHAVVGAAGADWAGGFLDLKADLQDPTFIGNELTPEVPAQYIGYVTVWLPSRQKTSLL 337  
Qy 421 ASGA PRYOHMGRVLLFQEPQGGHMSOVQTHGQISYSGELCGVDVDDGETELLII 480  
Db 338 ASGA PRYOHMGRVLLFQEPQGGHMSOVQTHGQISYSGELCGVDVDDGETELLII 397  
Qy 481 GAPFYGORGGRFYIQRQLGFEVSELSQDGPYLGREGALITALTIDNGGLVDVA 540  
Db 398 GAPFYGORGGRFYIQRQLGFEVSELSQDGPYLGREGALITALTIDNGGLVDVA 457  
Qy 541 VGAPLEEGAVYIFNGRHGGLSPQSORIESTQVLSGIQWFGRSIHGVKDLBGGDLADVA 600  
Db 458 VGAPLEEGAVYIFNGRHGGLSPQSORIESTQVLSGIQWFGRSIHGVKDLBGGDLADVA 517  
Qy 601 VGASQMI VLSRPVDMVTLMSPSPAPIPVHVEECYSYTSNNKKEGVNITTCQIKSLY 660  
Db 518 VGASQMI VLSRPVDMVTLMSPSPAPIPVHVEECYSYTSNNKKEGVNITTCQIKSLY 577  
Qy 661 PFGQRLVANLTYTLQDGHRTRRGLFPGGRHRLRNIAVTTSMSCDPSFHPVPCVOD 720  
Db 578 PFGQRLVANLTYTLQDGHRTRRGLFPGGRHRLRNIAVTTSMSCDPSFHPVPCVOD 637  
Qy 721 LISPINVS LPSLMBEERTPRDRAQKDIPIILRPSLHSETWEIPEKNCGEDKCCAN 780  
Db 638 LISPINVS LPSLMBEERTPRDRA -GKDIPIILRPSLHSETWEIPEKNCGEDKCCAN 696  
Qy 781 LRVSPARSALRLTAFASLVELSLNSLEBDAYVQDLHFRPPGLSPKVEMLKPHSQ 840

Db 697 LRVFSFSPARSLRLTAVASLSVSLSNLEEDAYWQJDLHPFGLSFRKVEMLKPHSQ 756  
Qy 841 I PVSCEBLPEBSRLSLRSLSCNVSPIFKAGHSVALQMMENTIVNNSGDSVEIHAANTC 900  
Db 757 I PVSCEBLPEBSRLSLRSLSCNVSPIFKAGHSVALQMMENTIVNNSGDSVEIHAANTC 816  
Qy 901 NNEBSDLLEDSNATTTIPIILYPINILIODQEDSTLYVSFTPKGPKIHQVKMYQVRIQPS 960  
Db 817 NNEBSDLLEDSNATTTIPIILYPINILIODQEDSTLYVSFTPKGPKIHQVKMYQVRIQPS 876  
Qy 961 IHDNIPLEAVVGVPPSPSGPTTHQMSVQMEPPVPCHYEDLERLPAAEPCLPGALFR 1020  
Db 877 IHDNIPLEAVVGVPPSPSGPTTHQMSVQMEPPVPCHYEDLERLPAAEPCLPGALFR 936  
Qy 1021 CPVVPROELIYOVLGTELVGEITEASSMFSICSLSTISFNSSKPHHLXGNSASIAQVVMK 1080  
Db 937 CPVVPROELIYOVLGTELVGEITEASSMFSICSLSTISFNSSKPHHLXGNSASIAQVVMK 996  
Qy 1081 VDVPYERQMLLYLVLSGIGLLLLIPIVLKYVFFGRNLKEKMEAGRGVPGNIPABDS 1140  
Db 997 VDVPYERQMLLYLVLSGIGLLLLIPIVLKYVFFGRNLKEKMEAGRGVPGNIPABDS 1056  
Qy 1141 EQLASGOEAGDPGCKLPHEKDSBSGGKGD 1170  
Db 1057 EQLASGOEAGDPGCKLPHEKDSBSGGKGD 1086

## RESULT 12

PCT-US05-02350-80  
; Sequence 80, Application PC/TUS0502350  
; GENERAL INFORMATION:  
; APPLICANT: Avalon-Soffer, Michal  
; APPLICANT: Levine, Zurit  
; APPLICANT: Sella-Tavor, Osnat  
; APPLICANT: Diber, Alex  
; APPLICANT: Shemesh, Ronen  
; APPLICANT: Toporik, Amir  
; APPLICANT: Rotman, Galit  
; APPLICANT: Nemzer, Sergey  
; APPLICANT: Rosenberg, Avi  
; APPLICANT: Dahanay, Dvir  
; APPLICANT: Wool, Assaf  
; APPLICANT: Cojocaru, Gad S.  
; APPLICANT: Akiva, Pinchas  
; APPLICANT: Pollock, Sarah  
; APPLICANT: Savitsky, Kimeret  
; APPLICANT: Bernstein, Jeanne  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES ENCODING POLYPEPTIDES AND METHODS USING  
; FILE REFERENCE: 28487  
; CURRENT APPLICATION NUMBER: PCT/US05/02350  
; CURRENT FILING DATE: 2005-02-10  
; NUMBER OF SEQ ID NOS: 1155  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 80  
; LENGTH: 750  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US05-02350-80

Query Match 63.6%; Score 3885; DB 1; Length 750;  
Best Local Similarity 99.5%; Pred. No. 5.6e-287;  
Matches 745; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MKDCITVMAMALLSGFFFPASSYNLDVGARSPSPARRHFGYRVLVQNGVTVGA 60  
Db 1 MKDCITVMAMALLSGFFFPASSYNLDVGARSPSPARRHFGYRVLVQNGVTVGA 60  
Qy 61 PGBENSTGSLYQCCSGGCHCLPYTLRGANTSKYLQMTLADPTDGSGLIADCPGLSTCD 120  
Db 61 PGBENSTGSLYQCCSGGCHCLPYTLRGANTSKYLQMTLADPTDGSGLIADCPGLSTCD 120

Qy 121 QNTYLSGLCYLFRONTLOGPMLQGRPGFOECIKGNVDLVFLPDSMSLQDEFOKILDFMK 180  
Db 121 QNTYLSGLCYLFRONTLOGPMLQGRPGFOECIKGNVDLVFLPDSMSLQDEFOKILDFMK 180  
Qy 181 DVMKLSNTSYQPAVQFSTSYTEPDSYVYRKQDPDALLKIVKMLLTNTFGAINV 240  
Db 181 DVMKLSNTSYQPAVQFSTSYTEPDSYVYRKQDPDALLKIVKMLLTNTFGAINV 240  
Qy 241 ATEVFRBELGARPATVLLIITDGEATDSGNIDAAKDIIIRYIIIGKHPQTESQETLH 300  
Db 241 ATEVFRBELGARPATVLLIITDGEATDSGNIDAAKDIIIRYIIIGKHPQTESQETLH 300  
Qy 301 KFASKPASEFVKILDPTEKLDLFTTELQKKIYIYEGTSKODLTSFNNELSSSGISADLSR 360  
Db 301 KFASKPASEFVKILDPTEKLDLFTTELQKKIYIYEGTSKODLTSFNNELSSSGISADLSR 360  
Qy 361 GHAVVAGAKDMAAGFLDLKADLODDTFI GNEPLTPEVAGYLYGVVTLPSRQKTSLL 420  
Db 361 GHAVVAGAKDMAAGFLDLKADLODDTFI GNEPLTPEVAGYLYGVVTLPSRQKTSLL 420  
Qy 421 ASGAPRYQHMGRVLLPQEPQGGHMSQVOTIHGTQISYRFGELCGVDVQDDETELLI 480  
Db 421 ASGAPRYQHMGRVLLPQEPQGGHMSQVOTIHGTQISYRFGELCGVDVQDDETELLI 480  
Qy 481 GAPLFYGBQRGVFTIYQRRQLGFEVSELOQDPYPLGRFGAITLTDINGDLVDA 540  
Db 481 GAPLFYGBQRGVFTIYQRRQLGFEVSELOQDPYPLGRFGAITLTDINGDLVDA 540  
Qy 541 VGAPLEQGAIVYIFNGRHGSLSPQSORITGTVLSGIQMFGRSIGHVKDLBEDGLADVA 600  
Db 541 VGAPLEQGAIVYIFNGRHGSLSPQSORITGTVLSGIQMFGRSIGHVKDLBEDGLADVA 600  
Qy 601 VGASQMTVLSR PVDVMTLMSFSPAETPVHVECSYTSNMOKGWNITTFQIKSLY 660  
Db 601 VGASQMTVLSR PVDVMTLMSFSPAETPVHVECSYTSNMOKGWNITTFQIKSLY 660  
Qy 661 POFQGRVLANITYTLQDGHRTRRRGLFPGRHELRNLIATVTSMSCTDPSFFPVCVOD 720  
Db 661 POFQGRVLANITYTLQDGHRTRRRGLFPGRHELRNLIATVTSMSCTDPSFFPVCVOD 720  
Qy 721 LISFINVSLNFSLWEEGTPTDQDQAGKD 749  
Db 721 LISFINVSLNFSLWEEGTPTDQDQAVARD 749

## RESULT 13

US-11-043-770-80  
; Sequence 80, Application US/11043770  
; GENERAL INFORMATION:  
; APPLICANT: Avalon-Soffer, Michal  
; APPLICANT: Levine, Zurit  
; APPLICANT: Sella-Tavor, Osnat  
; APPLICANT: Diber, Alex  
; APPLICANT: Shemesh, Ronen  
; APPLICANT: Toporik, Amir  
; APPLICANT: Rotman, Galit  
; APPLICANT: Nemzer, Sergey  
; APPLICANT: Rosenberg, Avi  
; APPLICANT: Dahanay, Dvir  
; APPLICANT: Wool, Assaf  
; APPLICANT: Cojocaru, Gad S.  
; APPLICANT: Akiva, Pinchas  
; APPLICANT: Pollock, Sarah  
; APPLICANT: Savitsky, Kimeret  
; APPLICANT: Bernstein, Jeanne  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES ENCODING POLYPEPTIDES AND METHODS USING  
; FILE REFERENCE: 28488  
; CURRENT APPLICATION NUMBER: US/11/043,770  
; CURRENT FILING DATE: 2005-01-27  
; NUMBER OF SEQ ID NOS: 1155  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 80

LENGTH: 750  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-11-043-770-80

Query Match 63.6%; Score 3885; DB 7; Length 750;  
 Best Local Similarity 99.5%; Pred. No. 5.6e-287;  
 Matches 745; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

QY 1 MKDSCITTMAMALLSGFFFPAPASSYNDVRGANSFSPRRGRHFGYVLOVANGVIYGA 60
DB 1 MKDSCITTMAMALLSGFFFPAPASSYNDVRGANSFSPRRGRHFGYVLOVANGVIYGA 60
QY 61 PGEBSSTSLVQCCSGTGCHCLPVLIRGSNTYSKYLGMTLATPDGSLIACDPGSRICD 120
DB 61 PGEBSSTSLVQCCSGTGCHCLPVLIRGSNTYSKYLGMTLATPDGSLIACDPGSRICD 120
QY 121 QNTYLSGLCYLFRONLQGPMLQGRPGFQECIKANVDLFLFDGSMSLQDFQKILDPMK 180
DB 121 QNTYLSGLCYLFRONLQGPMLQGRPGFQECIKANVDLFLFDGSMSLQDFQKILDPMK 180
QY 181 DVMKLSNTSYQFAAVQSTSYKTEFDSYVKRDPALLKHVGMILLNTFGAINVY 240
DB 181 DVMKLSNTSYQFAAVQSTSYKTEFDSYVKRDPALLKHVGMILLNTFGAINVY 240
QY 241 ATEVPRELGRPADTKYLIIITDGEATDSGNIDAADIIIRYIIGIGHFQTKESQETLH 300
DB 241 ATEVPRELGRPADTKYLIIITDGEATDSGNIDAADIIIRYIIGIGHFQTKESQETLH 300
QY 301 KEASPKASEFVKILDTFEKLDLFTLQKIIYVIGTSKODLTSFNMELSSSGISADLSR 360
DB 301 KEASPKASEFVKILDTFEKLDLFTLQKIIYVIGTSKODLTSFNMELSSSGISADLSR 360
QY 361 GHAVGAVGADWAGFLDLKADLDDDTFIGNELTPERVAGYLGYYTWMPSRQKISL 420
DB 361 GHAVGAVGADWAGFLDLKADLDDDTFIGNELTPERVAGYLGYYTWMPSRQKISL 420
QY 421 ASQAPRYHMGVLLFQEPQGGHWSQVTHGTQISYFGGELCGVDVDDGETELLII 480
DB 421 ASQAPRYHMGVLLFQEPQGGHWSQVTHGTQISYFGGELCGVDVDDGETELLII 480
QY 481 GAFPEYGBORGRVFIYORROLGFEVSELQDPPYPLGRFGEAITALTIDINGDLVDA 540
DB 481 GAFPEYGBORGRVFIYORROLGFEVSELQDPPYPLGRFGEAITALTIDINGDLVDA 540
QY 541 VGAPLEEGAVYIFNGRHGGLSPQPSQRIEGTVLSGIQWFGRSIHGVKDLBGDLADVA 600
DB 541 VGAPLEEGAVYIFNGRHGGLSPQPSQRIEGTVLSGIQWFGRSIHGVKDLBGDLADVA 600
QY 601 VGABSQMTVLSRPVVDVMTLMSFPAIPVHEVECSYSTSNKMEGVNITTCFOIKSLI 660
DB 601 VGABSQMTVLSRPVVDVMTLMSFPAIPVHEVECSYSTSNKMEGVNITTCFOIKSLI 660
QY 661 POFQRLVANTTYTLQLDGHRTRRGLFPGGRHELRNIAVTTSMSCDPSFHPVCVD 720
DB 661 POFQRLVANTTYTLQLDGHRTRRGLFPGGRHELRNIAVTTSMSCDPSFHPVCVD 720
QY 721 LISPIVSLNFSLWEEGTPRDQAGKD 749
DB 721 LISPIVSLNFSLWEEGTPRDQAGKD 749

```

RESULT 14  
 US-11-062-290-2  
 Sequence 2, Application us/11062290  
 GENERAL INFORMATION:  
 APPLICANT: KAPUSTAY, PAMELA M.  
 TITLE OF INVENTION: LFA-1 ALPHA SUBUNIT ANTIBODIES AND METHODS OF USE  
 FILE REFERENCE: 046007/0272304  
 CURRENT APPLICATION NUMBER: US/11/062,290  
 CURRENT FILING DATE: 2005-02-17  
 PRIOR APPLICATION NUMBER: US/10/261,164

PRIOR FILING DATE: 2002-09-27  
 NUMBER OF SEQ ID NOS: 3  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 2  
 LENGTH: 589  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-11-062-290-2

Query Match 50.2%; Score 3066; DB 7; Length 589;  
 Best Local Similarity 99.8%; Pred. No. 9.6e-225;  
 Matches 589; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 26 YNLVDRARSPPRARHFGYRVLQVNGVIYGAPEBGNSTSLVQCCSGTGCHCLPVL 85
DB 1 YNLVDRARSPPRARHFGYRVLQVNGVIYGAPEBGNSTSLVQCCSGTGCHCLPVL 85
QY 86 RGSNTYSKYLGMTLATPDGSLIACDPGSRICDQNTYLSGLCYLFRONLQGPMLQGRP 145
DB 86 RGSNTYSKYLGMTLATPDGSLIACDPGSRICDQNTYLSGLCYLFRONLQGPMLQGRP 145
QY 146 GFQECIKANVDLFLFDGSMSLQDFQKILDPMKDVMKLSNTSYQFAAVQSTSYKTE 205
DB 146 GFQECIKANVDLFLFDGSMSLQDFQKILDPMKDVMKLSNTSYQFAAVQSTSYKTE 205
QY 206 FDSYDYVKRDPALLKHVGMILLNTFGAINVATEVPRELGRPADTKYLIIITDG 265
DB 206 FDSYDYVKRDPALLKHVGMILLNTFGAINVATEVPRELGRPADTKYLIIITDG 265
QY 266 EATDSGNIDAADIIIRYIIGIGHFQTKESQETLHKEASPKASEFVKILDTFEKLDLFT 325
DB 266 EATDSGNIDAADIIIRYIIGIGHFQTKESQETLHKEASPKASEFVKILDTFEKLDLFT 325
QY 326 ELQKKIYVIGTSKODLTSFNMELSSSGISADLSRGAHVAVGADWAGFLDLKADLQ 385
DB 326 ELQKKIYVIGTSKODLTSFNMELSSSGISADLSRGAHVAVGADWAGFLDLKADLQ 385
QY 386 DDTFIGNELTPERVAGYLGYYTWMPSRQKISLASGARPYOMGVLLFQEPQGGHWS 445
DB 386 DDTFIGNELTPERVAGYLGYYTWMPSRQKISLASGARPYOMGVLLFQEPQGGHWS 445
QY 446 SQVTHGTQISYFGGELCGVDVDDGETELLIIGAPLFYGBORGRVFIYORROLGFE 505
DB 446 SQVTHGTQISYFGGELCGVDVDDGETELLIIGAPLFYGBORGRVFIYORROLGFE 505
QY 506 EVSELQDPPYPLGRFGEAITALTIDINGDLVDAVGAPLEEGAVYIFNGRHGGLSPQ 565
DB 506 EVSELQDPPYPLGRFGEAITALTIDINGDLVDAVGAPLEEGAVYIFNGRHGGLSPQ 565
QY 566 SQRIEGTVLSGIQWFGRSIHGVKDLBGDLADVAVGABSQMTVLSRP 614
DB 566 SQRIEGTVLSGIQWFGRSIHGVKDLBGDLADVAVGABSQMTVLSRP 614

```

RESULT 15  
 US-60-651-235-76  
 Sequence 76, Application us/60651235  
 GENERAL INFORMATION:  
 APPLICANT: JOSELOFF, Elizabeth et al.  
 TITLE OF INVENTION: LUNG DISEASE TARGETS AND USES THEREOF  
 FILE REFERENCE: C0001581  
 CURRENT APPLICATION NUMBER: US/60/651,235  
 NUMBER OF SEQ ID NOS: 3512  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 76  
 LENGTH: 1153  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-60-651-235-76

Query Match 25.6%; Score 1564; DB 8; Length 1153;  
 Best Local Similarity 34.3%; Pred. No. 7e-110;

Matches 409; Conservative 212; Mismatches 464; Indels 108; Gaps 38;

```

Qy 6 ITWAMALLSGFFPAPASYNLDVRCARSPSPRAGHFGRYLV- GNCVIGABE- 63
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 6 LILNALITLCHG-----NLDENAMTFQ--BNAGFGQSVVQLGSSVVGAPDEI 54

Qy 64 --GNSGSLVYCCSGGTGCHLPVTLR-GSNYTSKYLGMATLADPTDGSILACDPGLSRTCD 120
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 55 VAAHQRGSLVYCCDYSTGCEPIRLQVPEAVNMISLGLSLAATSPQQLAGPVTYHQCS 114

Qy 121 QNTLSGLCYLFRONLQCPMLQGRPGFQECIKG---NVDLVFLFDGSMISLQDPFQKIL 176
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 115 ENTIVYKGLCFLFGSNLR---QOPQKPEALRGCPQEDSDIAFLIDSGSIIPHDFRMRK 170

Qy 177 DEMKQVMKLSNTSYQFAAYOESTSYKTEPFDSPDYKRDPAALLKHVHMLLLTNPFGA 236
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 171 EFVSTVMEQLKSKSLTBSLMQYSEBFRIHFTFKEPONNPNRSLVKPITQLGRTHATYG 230

Qy 237 INVAATEVFEELGARPDPATKVLIIITDGE--ATDSGNIDAKD-----IIRYIIGIKH 289
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 231 IRKTVRELFINTGARKAKAFKILVITDGEKFGDPLGYEDVLPBADREGVIRYIVGVDA 290

Qy 290 FQTESEOTLHKFASKRPASEFVKILDTPEKLDLTELQKTIYIEGTSKODLTSFMNEL 349
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 291 FRSEKSRQELNTTASKEPRDHVFQVNNFEALKTIQNLREKIFALBGTQTSSSSFEHEM 350

Qy 350 SSS$ISADLSRGHVVGAADWAGFLDKADLDODTFIGNEPLTPEVAGYLYTVT 409
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 351 SQEFSAITNGSLSTVGSYDNAGYF-LYTSKEKSTFTNMTRVDSMDNDATLGYAAA 409

Qy 410 WLPFRQKTSLLASGAPRYQHGKRVLLFQEPQGGHMSQVOTIHGTQIGSYFGELCGVDV 469
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 410 -IIRNRVQSLVLAGAPRYQHIGLVAMFR--QNTGMMESNANVKGTOIGAYFGASLCSVDV 466

Qy 470 DQDETBELLIGAPLYFYEGORGRVITY----QRQUGFEVSELOQDPGYPLRGSEA 524
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 467 DSNSTDLVLLGAPHYEQTRGGVSVCLPRGQARWQCDAY--LYGEOQGPWGRFGAA 524

Qy 525 ITALTIDINGDLVNVAVGAPLEB--OGAVYIFNGRHG-GLSPQSORIEGTQVLSGIOWF 581
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 525 LTVAGDVAGDCLTVAGAPBEEDNRGANVLPFGTSGSGISPSHSQRIAGSKLSPRLQYF 584

Qy 582 GRSIHGVNLEGGDLADVAVGAEQOMIVLSRPVVDVTLTMSFPAEIPVHEVECSYSTS 641
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 585 GQSLSGQDGLTMDGLVLDLVGAQGHVLLRSQPVLRVKAIMEFNPBEVABRVFECNDQV 644

Qy 642 NKATGCVNITTCFOI-KSLYPOF-OGRLVNLTYTLQLDGHRTRRGLFPGGRHRLRNT 699
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 645 -KGEABEVRVCLHVQKSTRDLRBEQIQSVVYVDLALDSGRPHSRVAFNETKNSTRQT 703

Qy 700 AVT-TSMSCDTFSFHPVCOVODLISPIVNSLNFSLMEEBGTPRDQAGKDIPLLRPSL 758
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 704 QVLELTQTCETLKLQLPNCIEDPVPSPYLRNLSI--VGTPLS--AFGN-----LRPVL 753

Qy 759 HSEIWEI-----PEKQCGEDKCEANLRVSPSPARSRLRLTAASLVELSLNLEED 813
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 754 AEDAQRLEFALPPEKQCGANDNICODDLSTFSFMSLDCLVVGGBRENFVTVVRNDEED 813

Qy 814 AYWQOLHLPFGSLSPKRVEML--KHSQIPVSCBEL--PEESRLSRALSCNVSSPIF 868
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 814 SYRQVTFEFPPLDSTYRKVSTLQNRQSRWRLCESASSTEVSGVL-KSTSCSINHPIF 872

Qy 869 KAGSHVALQMMFNTLVNNSMGDSVELHANVTCNNEDSDLEDNSATYI--IPLIYPINI 925
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 873 PENSEVTFNITFDVDSKASLQNLKILKANVTSENN---MPTNKTEPQLELPVKTAYTM 928

Qy 926 LIQDQEDSTLYVSFTPKGPKIHQVKMYOVRIOPSIHDPNIPTEAVVGVQPPSEGPIT 985
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 929 VVTSHGVSSTKYLNTFASENTSRVMQHQYV--SNLQGRSLP-ISLVFLVVRNLNQYIWM 984

Qy 986 HQMSVQMEPPV--FCHYEDLERLPDAAPCPLGALFRCFVV-----F 1025
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 985 DRPQVTESENLSYCHTK--ERLPSHSD--FLAEIRKAPVNCISIAVCORIQCDIPFPGI 1040

```

```

Qy 1026 ROELIVQVIGTLELVGEIRAS-SMFSLSSLSISFNSSKRHFLYGSNAPL-AQVMKVVDV 1083
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1041 QEBFNATLKGNLSFDWYIKTSHHLLIVSTAELFNDVSFTLLPGQAFVRSQTEYTER 1100

Qy 1084 VYRKQMLYLVLSGIGGLLLLIIFVLVYGVFPKRLKERMAGRGVNGIP 1136
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1101 FEVDPNPLPLIVGSSVGGLLLLALITLALVYKLGFPKQYKDMSEBG--GPPGAP 1152

```

Search completed: August 29, 2005, 19:37:09  
 Job time : 92 secs